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OM protein - protein search, using sw model

Run on: April 1, 2005, 12:33:12 ; Search time 181 Seconds

(without alignments)

1788.500 Million cell updates/sec

Title: US-09-634-287E-2

Perfect score: 4570

Sequence: 1 MSQTGSHPQRGLAGRMLMGA.....LHRRAQILEILRRRPWAGRK 837

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing First 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqD1900s:*

2: geneseqD1990s:*

3: geneseqD2000s:*

4: geneseqD2001s:*

5: geneseqD2002s:*

6: geneseqD2003ab:*

7: geneseqD2003bs:*

8: geneseqD2004s:*

RESULT 1
 AAW75425

ID AAW75425 standard; protein; 837 AA.

XX AAW75425;

XX DT 30-MAR-1999 (first entry)

XX DE Human aggrecan degrading metalloprotease 1.

XX KW Human; aggrecan degrading metalloprotease; cartilage; proteoglycan;

KW interglobular domain; matrix metalloprotease bovine; interleukin-1beta;

KW primer; PCR; amplification; inhibitor; cleavage; inhibitor; ADMP-1;

KW arthritis; joint injury; Pseudogout.

XX OS Homo sapiens.

XX PN WO9905291-A2.

XX PD 04-FEB-1999.

XX XX 24-JUL-1998; 98WO-US015438.

XX XX 25-JUL-1997; 97US-0053050P.

PR PR 15-AUG-1997; 97US-0055336P.

PR PR 16-OCT-1997; 97US-0062469P.

XX (DUPRO) DU PONT PHARM CO

PA PA Arner EC, Burn TC, Copeland RA, Decicco CP, Liu R, Magolda RL,

PI Pratta M, Solomon KA, Tortorella MD, Tortorella

XX DR WPI: 1999-14293/12.

DR N-PSDB; AAX00725.

XX XX Claim 25; Page 61-62; 73pp; English.

XX This sequence represents the human aggrecan degrading metalloprotease 1

CC (ADMP-1). ADMP-1 and ADMP-2 (AAW75425) are novel proteases that cleave

CC the aggrecan (a major cartilage proteoglycan) between residues Glu373-

CC Ala374 of the interglobular domain (compared with cleavage between

CC Phe342 by the matrix metalloproteases MMP-1, -2, -3, -7, -8, -9 and -

CC 13). ADMP-1 and ADMP-2 were isolated and purified from the conditioned

CC media of bovine nasal cartilage stimulated by interleukin-1beta. The

CC

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	4570	100.0	837 2 AAW75425	Aaw75425 Human agg
2	4570	100.0	837 7 ADJ69542	Adj69542 Human agg
3	4570	100.0	837 8 ADs20209	AdS20209 Human agg
4	4567	99.9	846 8 ADs20232	AdS20232 Human agg
5	4566	99.9	837 4 AAG78228	AAG78228 Human agg
6	4566	99.9	837 7 ADs85488	AdS85488 Human agg
7	4566	99.9	840 3 ABB21256	ABB21256 Human met
8	4563	99.8	837 3 AAY99429	AAY99429 Human PRO
9	4563	99.8	837 4 AABs6178	AABs6178 Protein O
10	4563	99.8	837 4 AAB29199	AAB29199 Human PRO
11	4563	99.8	837 6 ABUS8575	ABUS8575 Human PRO
12	4563	99.8	837 6 AB088123	Abu88123 Novel hum
13	4563	99.8	837 6 AB084438	Abu84438 Human sec
14	4563	99.8	837 6 ABB66313	Abr66313 Human sec
15	4563	99.8	837 6 ABB65702	Abr65702 Human sec
16	4563	99.8	837 6 AB099642	Abu99642 Human sec
17	4563	99.8	837 6 AB092881	Abu092881 Human PRO
18	4563	99.8	837 6 AB090002	Abu090002 Novel hum
19	4563	99.8	837 6 AB068251	Abu68251 Human sec
20	4563	99.8	837 6 AB096304	Abu96304 Novel hum
21	4563	99.8	837 6 AB092735	Abu92735 Human sec
22	4563	99.8	837 6 AB008812	Ab008812 Human sec
23	4563	99.8	837 6 AB002864	Ab002864 Human sec
24	4563	99.8	837 6 ABR75018	Abr75018 Human sec
25	4563	99.8	837 6 ABR94780	Abr94780 Human sec

* SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	4570	100.0	837 2 AAW75425	Aaw75425 Human agg
2	4570	100.0	837 7 ADJ69542	Adj69542 Human agg
3	4570	100.0	837 8 ADs20209	AdS20209 Human agg
4	4567	99.9	846 8 ADs20232	AdS20232 Human agg
5	4566	99.9	837 4 AAG78228	AAG78228 Human agg
6	4566	99.9	837 7 ADs85488	AdS85488 Human agg
7	4566	99.9	840 3 ABB21256	ABB21256 Human met
8	4563	99.8	837 3 AAY99429	AAY99429 Human PRO
9	4563	99.8	837 4 AABs6178	AABs6178 Protein O
10	4563	99.8	837 4 AAB29199	AAB29199 Human PRO
11	4563	99.8	837 6 ABUS8575	ABUS8575 Human PRO
12	4563	99.8	837 6 AB088123	Abu88123 Novel hum
13	4563	99.8	837 6 AB084438	Abu84438 Human sec
14	4563	99.8	837 6 ABB66313	Abr66313 Human sec
15	4563	99.8	837 6 ABB65702	Abr65702 Human sec
16	4563	99.8	837 6 AB099642	Abu99642 Human sec
17	4563	99.8	837 6 AB092881	Abu092881 Human PRO
18	4563	99.8	837 6 AB090002	Abu090002 Novel hum
19	4563	99.8	837 6 AB068251	Abu68251 Human sec
20	4563	99.8	837 6 AB096304	Abu96304 Novel hum
21	4563	99.8	837 6 AB092735	Abu92735 Human sec
22	4563	99.8	837 6 AB008812	Ab008812 Human sec
23	4563	99.8	837 6 AB002864	Ab002864 Human sec
24	4563	99.8	837 6 ABR75018	Abr75018 Human sec
25	4563	99.8	837 6 ABR94780	Abr94780 Human sec

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

purified proteins were partially sequenced and primers were synthesised based on the resultant amino acid sequences (AX00727-X00732 for ADMP-1 and AX00733-X00736 for ADMP-2). These were used to isolate the corresponding genes from cDNA. The ADMP polypeptides can be used for identifying inhibitors of ADMP activity which would prevent cleavage of the aggrecan core protein, thereby decreasing the loss of aggrecan from cartilage. Such inhibitors can be used for treating diseases such as osteoarthritis, joint injury, reactive arthritis, acute pyrophosphate arthritis (pseudogout), psoriatic arthritis and juvenile rheumatoid arthritis.

61	IVPEEKINGSVLFPGAPARLLCRLQATGETLLEBLQDGVQEGLTVQLGQAPELIG	120	FT	Domain	FT	note= "Pro-peptide"
121	GABPGTYLTGTINGDPESVASHWMDGALLGHLYQYRGAEHLHQPLEGGTPNSAGGPAGHI	180	FT	Domain	FT	note = Metalloproteinase catalytic domain
121	GABPGTYLTGTINGDPESVASHWMDGALLGHLYQYRGAEHLHQPLEGGTPNSAGGPAGHI	180	FT	Domain	FT	note = Disintegrin-like domain
181	LRKSPASQGPMCNVKAPLGSPPRPRAKRASLSRVEVTLVADDKMAAPHGAGIKR	240	FT	Domain	FT	note = TSP-1 (thrombospondin type I) motif
181	LRKSPASQGPMCNVKAPLGSPPRPRAKRASLSRVEVTLVADDKMAAPHGAGIKR	240	FT	Cleavage-site	FT	note = Cysteine-rich domain
241	YLTVMAAAAKAFKHPSPTRNPYSLVYTRVLVILSGSGEBSQGPSSAACTLRSFCAWORGIN	300	FT	Domain	FT	note= "Auto-digestion cleavage site"
241	YLTVMAAAAKAFKHPSPTRNPYSLVYTRVLVILSGSGEBSQGPSSAACTLRSFCAWORGIN	300	FT	Cleavage-site	FT	note= "Auto-digestion cleavage site"
301	TBDSDSPDHDTAILFETRQLCGVSTCDTLMADVGTVCDPARSACIETDGLQSAFTAA	360	XX	XX	XX	note= "Auto-digestion cleavage site"
301	TBDSDSPDHDTAILFETRQLCGVSTCDTLMADVGTVCDPARSACIETDGLQSAFTAA	360	PN	XX	XX	
361	HELGIVPNMLDHSKPCISLNGPLSTSHVMAPIVMAHYDPEEPWSPCSARFTIDFLDNGY	420	PD	XX	XX	05-FEB-2004.
361	HELGIVPNMLDHSKPCISLNGPLSTSHVMAPIVMAHYDPEEPWSPCSARFTIDFLDNGY	420	PR	XX	XX	29-JUL-2003; 2003WO-US023484.
421	GHCLLDKPRAPLHLPLVTPPGKQYDADRCQQLTGFDPDSRPHCQLPLPPCPACALWCSGHILNCHA	480	XX	XX	XX	29-JUL-2002; 2002US-0398721P.
421	GHCLLDKPRAPLHLPLVTPPGKQYDADRCQQLTGFDPDSRPHCQLPLPPCPACALWCSGHILNCHA	480	PA	PA	PA	(AMHP) WYETH.
481	MCOTKHSPPWADGTPCGPQAQCMGCRCLIMDQLQDENTIPOAGGKPGWPGWGDSCRTCGGGV	540	PA	PA	PA	(CORC/) CORCORAN C J.
481	MCOTKHSPPWADGTPCGPQAQCMGCRCLIMDQLQDENTIPOAGGKPGWPGWGDSCRTCGGGV	540	PA	PA	PA	(PLAN/) FLANNERY C R.
481	MCOTKHSPPWADGTPCGPQAQCMGCRCLIMDQLQDENTIPOAGGKPGWPGWGDSCRTCGGGV	540	PA	PA	PA	(ZENG/) ZENG W.
541	QFSSRDRCTRVPVRNGGKYCEGRTRFRSNTEDCOPTSALTFRREEQAYNHRDTLDFKSF	600	PA	PA	PA	(RACT/) RACIE L A.
541	QFSSRDRCTRVPVRNGGKYCEGRTRFRSNTEDCOPTSALTFRREEQAYNHRDTLDFKSF	600	PA	PA	PA	(MCDO/) McDONAGH T.
601	PGPMDWVPRYTSVAPQDCKLTQARALGYYYLEPRVYDGTCPSCPDSSSVYQGRCTHA	660	PI	PI	PA	(FREE/) FREEMAN B A.
601	PGPMDWVPRYTSVAPQDCKLTQARALGYYYLEPRVYDGTCPSCPDSSSVYQGRCTHA	660	XX	XX	PA	(GEOR/) GEORGIADIS K E.
661	GDRIGIISKKEKDCKMYCGGDSGCKSKOSGSPKFRGYVNVVTPAGATHILVRQQNP	720	DR	XX	PA	(LAV/) LAVALLIE E R.
661	GDRIGIISKKEKDCKMYCGGDSGCKSKOSGSPKFRGYVNVVTPAGATHILVRQQNP	720	PS	XX	XX	Corcoran CJ, Flannery CR, Zeng W, Racie LA, McDonagh T;
721	GRHSIYIALKLPDGSYALNGEYTLMPSPTDVVLPGAVSLRYSGATAASBTLSGHGPLAQ	780	PS	XX	XX	Freeman BA, Georgiadis KE, Lavallie ER;
721	GRHSIYIALKLPDGSYALNGEYTLMPSPTDVVLPGAVSLRYSGATAASBTLSGHGPLAQ	780	CC	XX	XX	Example 6; SEQ ID NO 1; 117pp; English.
781	LTLQVLYAGNPQDTRLRYSEFVRPPTSTPRTFQDNLHRQATLIRRPRWAGRK	837	CC	XX	XX	New is isolated, modified ADAMTS4 (aggrecanase) protein with improved
781	LTLQVLYAGNPQDTRLRYSEFVRPPTSTPRTFQDNLHRQATLIRRPRWAGRK	837	CC	XX	CC	stability useful for identifying inhibitors of the enzyme activity for
DB	ADS20209 standard; protein; 837 AA.	XX	CC	XX	CC	treating aggrecanase-associated conditions, including Osteoarthritis.
DB	ADS20209;	XX	CC	XX	CC	The invention relates to a novel isolated, modified ADAMTS4 (a
DB	ADS20209 (first entry)	XX	CC	XX	CC	disintegrin-like and metalloprotease (reprolysin type) with
Qy	RESULT 3	XX	CC	XX	CC	thrombospondin type 1 motif 4) protein with improved stability compared
Qy	ADS20209	XX	CC	XX	CC	to a naturally occurring, full-length ADAMTS4 protein, where the modified
Qy	ADS20209;	XX	CC	CC	CC	protein differs from the naturally occurring, full-length ADAMTS4 protein
DB	18-NOV-2004 (first entry)	XX	CC	CC	CC	by at least one amino acid. ADAMTS proteins are a subfamily of zinc
DB	Human aggrecanase ADAMTS4 pro-protein.	XX	CC	CC	CC	metalloproteases and include aggrecanases amongst their members. The
DB	ADS20209	XX	CC	CC	CC	protein of the invention demonstrates osteopathic, antiinflammatory,
DB	ADS20209	XX	CC	CC	CC	antiarthritic, antiarthritic and cytostatic activities and may be useful
Qy	ADS20209 standard; protein; 837 AA.	XX	CC	CC	CC	for treating aggrecanase-associated conditions, including osteoarthritis,
Qy	ADS20209;	XX	CC	CC	CC	glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic
DB	18-NOV-2004 (first entry)	XX	CC	CC	CC	arthritis, periodontal disease and Crohn's disease. The current sequence
DB	Human aggrecanase ADAMTS4 pro-protein.	XX	CC	CC	CC	is that of the human aggrecanase ADAMTS4 pro-protein of the invention
DB	ADS20209	XX	CC	CC	CC	which is encoded by DNA located at chromosome 1q21-q23.
Qy	RESULT 3	XX	CC	CC	CC	Sequence 837 AA;
Qy	ADS20209	XX	CC	CC	CC	Query Match 100.0%; Score 4570; DB 8; Length 837;
Qy	ADS20209	XX	CC	CC	CC	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Qy	ADS20209;	XX	CC	CC	CC	Matches 837; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Db	18-NOV-2004 (first entry)	XX	CC	CC	CC	1 MSQTSSHPGRLAGWGAQPCLLPVLPSWLVLLLIAISLPSARLASPLPREE
Db	Human aggrecanase ADAMTS4 pro-protein.	XX	CC	CC	CC	1 MSQTSSHPGRLAGWGAQPCLLPVLPSWLVLLLIAISLPSARLASPLPREE
Qy	RESULT 3	XX	CC	CC	CC	61 IVFPKPLNGSVLPGSGAPARLCLRGAFETLLELQDGSQVEGLTVQYLGQAPELIG 120
Qy	ADS20209	XX	CC	CC	CC	61 IVFPKPLNGSVLPGSGAPARLCLRGAFETLLELQDGSQVEGLTVQYLGQAPELIG 120
Qy	ADS20209 standard; protein; 837 AA.	XX	CC	CC	CC	Key Peptide 1. 212
Qy	ADS20209;	XX	CC	CC	CC	Location/Qualifiers
DB	Human aggrecanase ADAMTS4 pro-protein.	XX	CC	CC	CC	FT

QY 121 GAAPGTYLTGTINGDPESVASYLHWDGGALIGVLYQYRGAEILHQLQPLEGGTPNSAGGGCAHII 180
 Db 121 GAAPGTYLTGTINGDPESVASYLHWDGGALIGVLYQYRGAEILHQLQPLEGGTPNSAGGGCAHII 180
 QY 181 LRRKSPASGGQPMCNVKAPLGSPSPRPRAKFASLRSRPFETLVLVADDKMAAFHAGLKR 240
 Db 181 LRRKSPASGGQPMCNVKAPLGSPSPRPRAKFASLRSRPFETLVLVADDKMAAFHAGLKR 240
 QY 241 YLTVMAAAAKAFKHPSTRNPVSLVTRVLIGSGBGPQVGPSSACTLRSFCAWORGLN 300
 Db 241 YLTVMAAAAKAFKHPSTRNPVSLVTRVLIGSGBGPQVGPSSACTLRSFCAWORGLN 300
 QY 301 TPEDSDPDPHDFTDAILFTQDLCGYSTCDTGLADGTYCDPAPRSACLAIVEDDGLQSOAFTAA 360
 Db 301 TPEDSDPDPHDFTDAILFTQDLCGYSTCDTGLADGTYCDPAPRSACLAIVEDDGLQSOAFTAA 360
 QY 361 HELGHVFNMLHDNSKPCISLNGPLSTSRRHMAPVMAHTDPEEPWSPCSPARFTIDFLDNGY 420
 Db 361 HELGHVFNMLHDNSKPCISLNGPLSTSRRHMAPVMAHTDPEEPWSPCSPARFTIDFLDNGY 420
 QY 421 GHCLDKPAPLAPLPVTPFGKDYADROQOLTFGPDSPRCPOLPPCAALWCSGHNLGHA 480
 Db 421 GHCLDKPAPLAPLPVTPFGKDYADROQOLTFGPDSPRCPOLPPCAALWCSGHNLGHA 480
 QY 481 MCQTKHSPWADGTPCGPAOACMGCRCLINDOLODFTNIPQAGGNGPMEGFWGDCSRITCGGV 540
 Db 481 MCQTKHSPWADGTPCGPAOACMGCRCLINDOLODFTNIPQAGGNGPMEGFWGDCSRITCGGV 540
 QY 541 QFSSRDCTRPVPVRNGGKVKYCEGRTRFRSNTEDCPTGSALTPREEQAAYNHRTDLFKSF 600
 Db 541 QFSSRDCTRPVPVRNGGKVKYCEGRTRFRSNTEDCPTGSALTPREEQAAYNHRTDLFKSF 600
 QY 601 PGPMWDWVPRYTGTAPDQCKLTCOARAGYYTYLEPRVTDGTPCSPSOSSVQYGRCHIA 660
 Db 601 PGPMWDWVPRYTGTAPDQCKLTCOARAGYYTYLEPRVTDGTPCSPDSSVQYGRCHIA 660
 QY 661 GCDRIGSRRKFDCMVCGDGSCKSOGSGSPXKFRYGNVNTIIPAGATHILVRQOQN P 720
 Db 661 GCDRIGSRRKFDCMVCGDGSCKSOGSGSPXKFRYGNVNTIIPAGATHILVRQOQN P 720
 QY 7221 GHRSTYLAKLKPDSYALNGEYTLMPSPDVTWLFGAVSRLRYSGATASETLSGSHGPLAQ P 780
 Db 7221 GHRSTYLAKLKPDSYALNGEYTLMPSPDVTWLFGAVSRLRYSGATASETLSGSHGPLAQ P 780
 QY 781 LTLQYLVANPQDTRLYRPFVPRPTSPSPRPTSPDMLHRRAQILETRRPMWAGRK 837
 Db 781 LTLQYLVANPQDTRLYRPFVPRPTSPSPRPTSPDMLHRRAQILETRRPMWAGRK 837

RESULT 4
 ADS20232 ID ADS20232 standard; protein; 846 AA.
 XX ADS20232;
 DT 18-NOV-2004 (first entry)
 XX Human aggrecanase ADAMTS4 mutant E362Q protein with FLAG tag.
 DB XX
 KW ADAMTS4; a disintegrin-like and metalloprotease; thrombospondin type 1 motif 4; metalloprotease; aggrecanase; osteoarthritic; antiinflammatory; joint; cyrostatic; osteoarthritis; glioma; cancer; inflammatory joint; rheumatoid arthritis; septic arthritis; periodontal; Crohn's disease; human; enzyme; chromosome 1q21-q23; FLAG tag; mutant; mutein.
 XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 PT Misc-difference 362
 FT /note= "Wild-type Glu substituted by Gln"
 FT /note= "FLAG tag"

FT Misc-difference 838; .846
 /note= "FLAG tag"
 FT XX
 PN WO2004011637-A2.
 XX 05-FEB-2004.
 PD XX
 PF 29-JUL-2003; 2003WO-US022484.
 XX
 PR 29-JUL-2002; 2002US-0398721P.
 XX
 PA (AMHP) WYETH.
 PA (CORC/) CORCORAN C. J.
 PA (FLAN/) FLANNERY C. R.
 PA (ZENG/) ZENG W.
 PA (RACI/) RACIE L. A.
 PA (MCDO/) McDONAGH T.
 PA (FREB/) FREEMAN B. A.
 PA (GEOR/) GEORGIADIS K. E.
 PA (LAVA/) LAVALLIE E. R.
 XX
 PI Corcoran CJ, Flannery CR, Zeng W, Racie LA, McDonagh T;
 PI Freeman BA, Georgiadis KE, Lavallie ER;
 XX
 DR WPI; 2004-143866/14.
 XX
 PT New isolated, modified ADAMTS4 (aggrecanase) protein with improved PT stability useful for identifying inhibitors of the enzyme activity for PT treating aggrecanase-associated conditions, including osteoarthritis.
 XX
 PS SEQ ID NO 29; 117pp; English.
 XX
 CC The invention relates to a novel isolated, modified ADAMTS4 (a
 CC disintegrin-like and metalloprotease (reprolyase) type
 CC thrombospondin type 1 motif 4) protein with improved stability compared
 CC to a naturally occurring, full-length ADAMTS4 protein, where the modified
 CC protein differs from the naturally occurring, full-length ADAMTS4 protein
 CC by at least one amino acid. ADAMTS proteins are a subfamily of zinc
 CC metalloproteases and include aggrecanases amongst their members. The
 CC protein of the invention demonstrates osteopathic, antiinflammatory,
 CC antiarthritic, antirheumatic and cyrostatic activities, and may be useful
 CC for treating aggrecanase-associated conditions, including osteoarthritis,
 CC glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic
 CC arthritis, periodontal disease and Crohn's disease. The current sequence
 CC tag of the human aggrecanase ADAMTS4 mutant E362Q protein with FLAG
 CC tag of the invention.
 XX
 SQ Sequence 846 AA;

Query Match 99.9%; Score 4567; DB 8; Length 846;
 Best Local Similarity 99.9%; P-reqd. No. 0; Indels 0; Gaps 0;
 Matches 836; Conservative 836;
 QY 1 MSQTGSHPGRGLAGRMWGAQPCLLPDPVLSWLVWVLLLILASLSPRPEEE 60
 Db 1 MSQTGSHPGRGLAGRMWGAQPCLLPDPVLSWLVWVLLLILASLSPRPEEE 60
 QY 61 IVPPERKINGSVLSGAPARLCLQAFGETLLELQDSGIVQEVTIVQIQQAPELLG 120
 Db 61 IVPPERKINGSVLSGAPARLCLQAFGETLLELQDSGIVQEVTIVQIQQAPELLG 120
 QY 121 GAFPGTYLTGTGTINGDPESVASHWDGGALLGIVLQYRGAEILHQLPLEGTPNSAGGPQAHII 180
 Db 121 GAFPGTYLTGTGTINGDPESVASHWDGGALLGIVLQYRGAEILHQLPLEGTPNSAGGPQAHII 180
 QY 181 LRRKSPASGQGPNCNTVKAPLGSPSPRPRAKFASLRSRPFETLVLVADDKMAAFHAGLKR 240
 Db 181 LRRKSPASGQGPNCNTVKAPLGSPSPRPRAKFASLRSRPFETLVLVADDKMAAFHAGLKR 240
 QY 241 YLLTVMAAAKAKAKHPSIRNPVSLVWVLSGEECPQVPSAAQTLRSFCAWQRGLN 300
 Db 241 YLLTVMAAAKAKAKHPSIRNPVSLVWVLSGEECPQVPSAAQTLRSFCAWQRGLN 300

XX	aggregcanase; aggrecan; articular cartilage; proteoglycan;	61	IVFPEELNGSVLPGSQGAPARLLCRLQAFETLLELDQSGVQEGLTVQYLGQAPELLG	120
KW	cartilage compressibility; elasticity; articular disease;	61	IVFPEELNGSVLPGSQGAPARLLCRLQAFETLLELDQSGVQEGLTVQYLGQAPELLG	120
KW	osteoarthritis; cartilage degeneration; inflammatory joint disease;	121	GAEPCTYLTGTGIDPESVASYLHWNDGALLQGTYRGAELHQLPDTGTPNSAGGPGAHI	180
KW	aggrecanase-1; ADAMTS-4; aggrecanase-2	121	GAEPCTYLTGTGIDPESVASYLHWNDGALLQGTYRGAELHQLPDTGTPNSAGGPGAHI	180
KW	TSR domain; osteopathic; antiarthritic; cytostatic; antiinflammatory;	121	GAEPCTYLTGTGIDPESVASYLHWNDGALLQGTYRGAELHQLPDTGTPNSAGGPGAHI	180
KW	antirheumatic; ophthalmological; thrombophilic; vasotropic; antimicrobial;			
KW	respiratory-gen; nootropic; neuroprotective; antiparkinsonian;			
KW	immunoexpressive; aggrecanase inhibition; cancer; rheumatoid arthritis;			
KW	septic arthritis; corneal ulceration; coronary thrombosis;			
KW	Crohn's disease; emphysema; Alzheimer's disease; Parkinson's disease;			
XX	multiple sclerosis; aortic aneurysm; enzyme; human.			
OS	Homo sapiens			
XX	W02003046822-A2.	241	YLLTYMAAAAKAFKHSISIRNFVSLVTRVLGSSEBGPVQYPSAATLRSFCAWQRGLN	300
PN		241	YLLTYMAAAAKAFKHSISIRNFVSLVTRVLGSSEBGPVQYPSAATLRSFCAWQRGLN	300
XX	14-AUG-2003.	361	HELGVFNMLHDNSKPCISLNGPLTSRHYMAPVNAHVDEBEPWNPSCSARFITDPLDNGY	420
PD		361	HELGVFNMLHDNSKPCISLNGPLTSRHYMAPVNAHVDEBEPWNPSCSARFITDPLDNGY	420
XX	05-FEB-2003; 2003WO-US003554.	301	TPEDSDPDHFDTAILFTRDLCVGVSTCDTGMDYGTCDPARSQAVEDGLOQAPTA	360
PF		301	TPEDSDPDHFDTAILFTRDLCVGVSTCDTGMDYGTCDPARSQAVEDGLOQAPTA	360
XX	PR: 2003-731495/69.	421	GHCLLDPPEAFLHLPPTPGKDYDARQCOLTGFPSRHCPCQLPSPCAALWCSGHINGHA	480
DR		421	GHCLLDPPEAFLHLPPTPGKDYDARQCOLTGFPSRHCPCQLPSPCAALWCSGHINGHA	480
XX	(ANHP) WYETH.	481	MCQTKHSPWADGTPCGPAQACNGRCLHMDQLQDFNIPQAGGWWGPWGDGCSRTGGVV	540
PA		481	MCQTKHSPWADGTPCGPAQACNGRCLHMDQLQDFNIPQAGGWWGPWGDGCSRTGGVV	540
XX	Georgiadis K, Crawford TK, Tomkinson KN, Morris EA, Racie L;	541	QFSSRQDCTPVERGNGCGRTRRSCTEDCPFGSALTFREECCTAHTHRDIFPKSF	600
PI		541	QFSSRQDCTPVERGNGCGRTRRSCTEDCPFGSALTFREECCTAHTHRDIFPKSF	600
XX	WPI: 2003-731495/69.	601	PGPMDWNPYRPTGVAQPDQCKLTQCARALGHYYVLEPRVDCTPCSDSSVYCOGRCIHA	660
DR		601	PGPMDWNPYRPTGVAQPDQCKLTQCARALGHYYVLEPRVDCTPCSDSSVYCOGRCIHA	660
XX	DR-25DB; ADB85504.	661	GCDRIGSKKEDKCMYCGDGSGCCQSGSFRKFRYGNVNTIPAGATHILVRQGNP	720
XX	New biologically-active aggrecanase protein having a deletion of all, or	661	GCDRIGSKKEDKCMYCGDGSGCCQSGSFRKFRYGNVNTIPAGATHILVRQGNP	720
PT	a portion of a TSR domain, useful for treating osteoarthritis, cancer,			
PT	Parkinson's disease, coronary thrombosis, Alzheimer's disease and			
PT	multiple sclerosis.			
XX	Disclosure; Fig 11; 111pp; English.			
PS				
XX	This invention relates to novel truncated human aggrecanase proteins and			
CC	nucleotide sequences. Aggrecan is a major extracellular component of			
CC	articular cartilage. It is a proteoglycan responsible for providing			
CC	elasticity with its mechanical properties of compressibility and			
CC	of articular cartilage in arthritic diseases such as osteoarthritis.			
CC	Aggrecanase is responsible for the cleavage of aggrecan, thereby having a			
CC	role in cartilage degradation associated with osteoarthritis and			
CC	inflammatory joint disease. The proteins of the current invention are			
CC	truncated aggrecanase-1 (ADAMTS-4) and aggrecanase-2 (ADAMTS-5) enzymes			
CC	which have at least one thrombospondin (TSP) domain deleted. These are			
CC	biologically active and have greater stability and higher expression than			
CC	their full-length counterparts. The proteins of the invention may be of			
CC	use in the development of compounds with osteoarthritis and			
CC	cystostatic, antiinflammatory, antirheumatic, ophthalmological,			
CC	neuroprotective, antimicrobial, immunosuppressive activities through			
CC	aggrecanase inhibition. The proteins of the invention may therefore be			
CC	useful for the manufacture of compositions for the treatment of			
CC	aggrecanase-associated conditions, such as osteoarthritis, cancer,			
CC	inflammatory joint disease, rheumatoid arthritis, septic arthritis,			
CC	corneal ulceration, coronary thrombosis, Crohn's disease, emphysema,			
CC	Alzheimer's disease, Parkinson's disease, multiple sclerosis and aortic			
CC	aneurysm. The present sequence is the full-length amino acid sequence of			
CC	the aggrecanase-1 (ADAMTS-4) enzyme which was used to create the			
CC	truncated aggrecanases-1 proteins of the invention.			
XX	Sequence 837 AA;			
SQ	Query Match 99.9%; Best Local Similarity 99.9%; Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Score 4566; DB 7; Length 837;		
XX	1 MSQTGSHPGRGLAGRMWGAQPCLLPPIVPLSWLWLLILASLSPSLPREE	Pred: No; AC		
XX	1 MSQTGSHPGRGLAGRMWGAQPCLLPPIVPLSWLWLLILASLSPSLPREE	Mismatches: 1; 23-FEB-2001 (first entry)		
XX	Db	XX	XX	
XX	Human metalloproteinase KIAA0688.			
KW	Human; KIAA0688; metalloproteinase; ADAM;			
KW	a disintegrin and metalloproteinase domain; cerebroprotective;			
KW	vaccine; nootropic; neuroprotective; anti-parkinsonian; cyclostatic;			
KW	antiarthritic; immunosuppressive; Alzheimer's disease; Parkinson's disease; stroke; arthritis; autoimmune disease;			
KW	brain tumour; brain injury.			
XX	Home sapiens.			

Db	301	TPEDSGPDHPDTAILFTRDLCGVGSTCDTLMADVGTVCDPARSACIIVEDDGLOSAFTAA	360	DR	WPI : 2001-071395/08.
Qy	361	HEIGHVFTMLHDNSKPCITSNLNGPLSTSRRHMAVPAVMAHVDPEEPWSPCSARFETTDFLDNGY	420	XX	Secreted and transmembrane proteins and nucleic acids designated PRO.
Db	361	HEIGHVFTMLHDNSKPCITSNLNGPLSTSRRHMAVPAVMAHVDPEEPWSPCSARFETTDFLDNGY	420	PT	PT useful as hybridization probes, in chromosome and gene mapping and gene
Qy	421	GHCILDKPRAPELHLPLTPEFGKDYDAEQRQCOLTTFGPDSERHCPOLPPPCAALMCSGHNLGHA	480	PT	therapy.
Db	421	GHCILDKPRAPELHLPLTPEFGKDYDAEQRQCOLTTFGPDSERHCPOLPPPCAALMCSGHNLGHA	480	XX	Claim 1; Fig 180; 787pp; English.
Qy	421	MCQTKHSKPWADGTPCPGAQACNGGRCLHMDQLODENPIQAGGWGPNGPWCSDRSGGGV	540	CC	The present invention relates to secreted and transmembrane proteins.
Qy	481	MCQTKHSKPWADGTPCPGAQACNGGRCLHMDQLODENPIQAGGWGPNGPWCSDRSGGGV	540	CC	These proteins and the DNA encoding them may be used as hybridization
Db	481	MCQTKHSKPWADGTPCPGAQACNGGRCLHMDQLODENPIQAGGWGPNGPWCSDRSGGGV	540	CC	probes, in chromosome and gene mapping and in the generation of anti-
Qy	541	OPSSRDCTRPVPRNGGKCYCEGRTRFRSNTEDCPTGSALTFREBOCAVNHRTDLFKSF	600	CC	sense RNA and DNA. They may also be used used to generate either
Db	541	OPSSRDCTRPVPRNGGKCYCEGRTRFRSNTEDCPTGSALTFREBOCAVNHRTDLFKSF	600	CC	transgenic animals or knockout animals which are in turn useful for
Qy	601	PGPMDWYVPRYTGTYWAPODQCKLTCQARALGTYVLEPRVVDGTPCSDSSVSYCQGRCIHA	660	CC	development and screening of therapeutically useful reagents. The nucleic
Db	601	PGPMDWYVPRYTGTYWAPODQCKLTCQARALGTYVLEPRVVDGTPCSDSSVSYCQGRCIHA	660	CC	acids may also be used in gene therapy.
Qy	661	GCDRITGSKKEPDCKMVGCGDSSGCKSOSGSPRKFRYGYNNVVTIPAGATHILVRQGNP	720	XX	Sequence 837 AA;
Db	661	GCDRITGSKKEPDCKMVGCGDSSGCKSOSGSPRKFRYGYNNVVTIPAGATHILVRQGNP	720	Qy	Query Match 99.8%; Score 4563; DB 4; Length 837;
Qy	721	GHRSTIYALAKLPDGSYAALNGEYTLMPSPDVTLPGAVSLRYSGATASSETLSGHGPLAQP	780	Db	Best Local Similarity 99.3%; Pred. No. 0; Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	721	GHRSTIYALAKLPDGSYAALNGEYTLMPSPDVTLPGAVSLRYSGATASSETLSGHGPLAQP	780	Qy	1 MSQTGSHPGRGLAGRMWGAOPCLLPIVPLSWLVLMLLILASLPSARLASPLPREE 60
Qy	781	LTLQVLYAGNPDTTRIYSSFFYPRPTSTPRPTPQDWLHRRAQILEILRREPWAGRK	837	Db	1 MSQTGSHPGRGLAGRMWGAOPCLLPIVPLSWLVLMLLILASLPSARLASPLPREE 60
Db	781	LTLQVLYAGNPDTTRIYSSFFYPRPTSTPRPTPQDWLHRRAQILEILRREPWAGRK	837	Qy	61 IVFPBKLGNSVLPGSGAPARLICRLOAFTLLEQBDQSGVQVEGLTVQYLQOAPFLLG 120
Qy	781	LTLQVLYAGNPDTTRIYSSFFYPRPTSTPRPTPQDWLHRRAQILEILRREPWAGRK	837	Db	61 IVFPBKLGNSVLPGSGAPARLICRLOAFTLLEQBDQSGVQVEGLTVQYLQOAPFLLG 120
Db	781	LTLQVLYAGNPDTTRIYSSFFYPRPTSTPRPTPQDWLHRRAQILEILRREPWAGRK	837	Qy	121 GABPGTYLTGTGNGDPEVASLHWGDGALIQLVQYGAELHQPLFEGTPNSAGGPGAH 180
Db	781	LTLQVLYAGNPDTTRIYSSFFYPRPTSTPRPTPQDWLHRRAQILEILRREPWAGRK	837	Db	121 GABPGTYLTGTGNGDPEVASLHWGDGALIQLVQYGAELHQPLFEGTPNSAGGPGAH 180
Qy	181	LRRKSPASGQCPMCNTKAPLQSPSPPRRAKRFASLSSRPTVTLWADDKMAAFHGAGLKR	240	Qy	181 LRRKSPASGQCPMCNTKAPLQSPSPPRRAKRFASLSSRPTVTLWADDKMAAFHGAGLKR 240
Db	181	LRRKSPASGQCPMCNTKAPLQSPSPPRRAKRFASLSSRPTVTLWADDKMAAFHGAGLKR	240	Db	181 LRRKSPASGQCPMCNTKAPLQSPSPPRRAKRFASLSSRPTVTLWADDKMAAFHGAGLKR 240
Qy	241	YLLTVNAAAATAKPHSIRNPVSLVYTRVLVIGSGEGBGPQVGPSSAQTLSFCAWQRLN	300	Qy	241 YLLTVNAAAATAKPHSIRNPVSLVYTRVLVIGSGEGBGPQVGPSSAQTLSFCAWQRLN 300
Db	241	TPEDSDPDHFDTAILFTRODLCGVSTCDTLMADYVSTVCDPASCSLIVEDDGLQSAFTAA	360	Db	241 TPEDSDPDHFDTAILFTRODLCGVSTCDTLMADYVSTVCDPASCSLIVEDDGLQSAFTAA 360
Qy	301	MCQTKHSKPWADGTPCSDPQACMGGRCLHMDQLODFENIPOAGCWGPNGPWCSDRSGGGV	480	Qy	301 TPEDSDPDHFDTAILFTRODLCGVSTCDTLMADYVSTVCDPASCSLIVEDDGLQSAFTAA 360
Db	421	GHCLLDKPPEAHLPLTFPGKDYDABRQCLTGFPSRHCFCQLPPGAALMCSGHNLGHA	480	Db	421 GHCLLDKPPEAHLPLTFPGKDYDABRQCLTGFPSRHCFCQLPPGAALMCSGHNLGHA 480
Qy	481	MCQTKHSKPWADGTPCSDPQACMGGRCLHMDQLODFENIPOAGCWGPNGPWCSDRSGGGV	540	Qy	481 MCQTKHSKPWADGTPCSDPQACMGGRCLHMDQLODFENIPOAGCWGPNGPWCSDRSGGGV 540
Db	481	MCQTKHSKPWADGTPCSDPQACMGGRCLHMDQLODFENIPOAGCWGPNGPWCSDRSGGGV	540	Db	481 MCQTKHSKPWADGTPCSDPQACMGGRCLHMDQLODFENIPOAGCWGPNGPWCSDRSGGGV 540
Qy	541	QFSSRDCTRPVRNGGKYCEGRTRRSNTEDCPGNSALTFRREEQCAAYNHRTDLFKSF	600	Qy	541 QFSSRDCTRPVRNGGKYCEGRTRRSNTEDCPGNSALTFRREEQCAAYNHRTDLFKSF 600
Db	541	QFSSRDCTRPVRNGGKYCEGRTRRSNTEDCPGNSALTFRREEQCAAYNHRTDLFKSF	600	Db	541 QFSSRDCTRPVRNGGKYCEGRTRRSNTEDCPGNSALTFRREEQCAAYNHRTDLFKSF 600
Qy	601	PGPMDWVPRYTGVAAPDQCKLTCQABALGYYVBLERVVDGTPCSDSSSVQGRCIHA	660	Qy	601 PGPMWVPRYTGVAAPDQCKLTCQABALGYYVBLERVVDGTPCSDSSSVQGRCIHA 660
Db	601	PGPMDWVPRYTGVAAPDQCKLTCQABALGYYVBLERVVDGTPCSDSSSVQGRCIHA	660	Db	601 PGPMDWVPRYTGVAAPDQCKLTCQABALGYYVBLERVVDGTPCSDSSSVQGRCIHA 660
PA	661	GCDRIGSKKKFDKCNVCGDGSCKSGSKFRKFRYGYNNVVTIPAGATHILVRQGNP	720	PA	(GETH) GENENTECH INC.
XX	661	GCDRIGSKKKFDKCNVCGDGSCKSGSKFRKFRYGYNNVVTIPAGATHILVRQGNP	720	XX	Baker KP , Botstein D , Desnoyers L , Eaton DL , Ferrara N , Fong S ,
PI	721	CHRSHYIALKLPDGSYALNGEYTLMPMSPTDVLLPGAVSLRYSGATAASETLSGHGPLAQ	780	PI	Gao W , Goddard A , Godowski PJ , Grimaldi CJ , Gurney AL , Hillian KJ ,
PI	721	CHRSHYIALKLPDGSYALNGEYTLMPMSPTDVLLPGAVSLRYSGATAASETLSGHGPLAQ	780	PI	Pan J , Paoni NF , Roy MA , Stewart TA , Tumas D , Watanabe CK , Williams PM , Wood WI ,
XX	721	CHRSHYIALKLPDGSYALNGEYTLMPMSPTDVLLPGAVSLRYSGATAASETLSGHGPLAQ	780	XX	

Qy	601	PGPMDDWVPRYTGVAPQDOCKLTCQARALGYYTYLEPRVVDGTPCSPDSSSVCVQGRCIHA	660	98US-0081195P.
Db	601	PGPMDDWVPRYTGVAPQDOCKLTCQARALGYYTYLEPRVVDGTPCSPDSSSVCVQGRCIHA	660	98US-008188P.
Qy	661	GCDRIIGSKKKPDKCMVCGDGGCSKOSGSFRKFRGYNNVTIPAGATHILVROQNP	720	98US-0082568P.
Db	661	GCDRIIGSKKKPDKCMVCGDGGCSKOSGSFRKFRGYNNVTIPAGATHILVROQNP	720	98US-0082104P.
Qy	721	GHSIYLALKLPPGSYALNGEYTLMPSPDTVVLPGAWSLRYSGATAASETLSGHGPLAQP	780	98US-0082737P.
Db	721	GHSIYLALKLPPGSYALNGEYTLMPSPDTVVLPGAWSLRYSGATAASETLSGHGPLAQP	780	98US-0083322P.
Qy	781	LTLQVLVAGNPOQTRLRYSFVPRPTSPTRPTPQDWLHRRAQILETRRWPWAGRK	837	98US-0083495P.
Db	781	LTLQVLVAGNPOQTRLRYSFVPRPTSPTRPTPQDWLHRRAQILETRRWPWAGRK	837	98US-0083466P.
Qy	781	LTLQVLVAGNPOQTRLRYSFVPRPTSPTRPTPQDWLHRRAQILETRRWPWAGRK	837	98US-0083499P.
Db	781	LTLQVLVAGNPOQTRLRYSFVPRPTSPTRPTPQDWLHRRAQILETRRWPWAGRK	837	98US-0083550P.
Qy	781	LTLQVLVAGNPOQTRLRYSFVPRPTSPTRPTPQDWLHRRAQILETRRWPWAGRK	837	98US-0084366P.
Db	781	LTLQVLVAGNPOQTRLRYSFVPRPTSPTRPTPQDWLHRRAQILETRRWPWAGRK	837	98US-0084414P.
Qy	781	LTLQVLVAGNPOQTRLRYSFVPRPTSPTRPTPQDWLHRRAQILETRRWPWAGRK	837	98US-0084630P.
Db	781	LTLQVLVAGNPOQTRLRYSFVPRPTSPTRPTPQDWLHRRAQILETRRWPWAGRK	837	98US-0084610P.
<hr/>				
RESULT 11				
AC	ABU58575	standard; protein; 837 AA.		98US-0084633P.
XX				98US-0084639P.
DT	15-APR-2003	(first entry)		98US-0084866P.
XX				98US-0085100P.
DE				98US-0085522P.
XX				98US-0086700P.
OS				98US-0086033P.
PN	US2003027272-A1.			98US-0086392P.
XX				98US-0087048P.
PD	06-FEB-2003.			98US-0087088P.
XX				98US-0087208P.
PP	06-JUN-2002;	2002US-00176492.		98US-0087208P.
XX				98US-008759P.
PR	03-JUN-1998;			98US-0087327P.
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PR	25-JUN-1998;			98US-0090630P.
PR	25-JUN-1998;			98US-0090694P.
PR	25-JUN-1998;			98US-0090659P.
PR	25-JUN-1998;			98US-0090656P.

KW tumour necrosis factor-alpha release; TNF-alpha release;
 KW chondrocyte proliferation; chondrocyte differentiation; tumour;
 KW adrenal tumour; lung tumour; colon tumour; breast tumour;
 KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

XX OS Homo sapiens.

XX US2003032127-A1.

XX PD 13-FEB-2003.

XX 26-JUN-2002; 2002US-00183012.

PP PR 18-SEP-1997; 97US-0059263P.

XX PR 18-SEP-1997; 97US-0059264P.

PR 17-OCT-1997; 97US-0062250P.

PR 21-OCT-1997; 97US-0063488P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 28-OCT-1997; 97US-0063540P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063544P.

PR 29-OCT-1997; 97US-0063564P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066120P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066734P.

PR 11-DEC-1997; 97US-0069335P.

PR 12-DEC-1997; 97US-0069425P.

PR 17-DEC-1997; 97US-0069870P.

PR 18-DEC-1997; 97US-0068017P.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077634P.

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PR 20-MAR-1998; 98US-0069335P.

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PR 27-MAR-1998; 98US-0078983P.

PR 08-APR-1998; 98US-0080104P.

PR 27-MAR-1998; 98US-0081070P.

PR 31-MAR-1998; 98US-0081070P.

PR 01-APR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080327P.

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PR 22-APR-1998; 98US-0082704P.

PR 05-APR-1998; 98US-0081070P.

PR 09-APR-1998; 98US-0081195P.

PR 28-APR-1998; 98US-0083322P.

PR 29-APR-1998; 98US-0083495P.

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PR 22-MAY-1998; 98US-0083453P.

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PR 22-MAY-1998; 98US-0086392P.

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PR 02-JUN-1998; 98US-0087609P.

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PR 04-AUG-1998; 98US-0091506P.

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PR 10-AUG-1998; 98US-0091748P.

PR 10-AUG-1998; 98US-009186P.

PR 10-AUG-1998; 98US-0091926P.

PR 10-AUG-1998; 98US-0091933P.

PR 10-AUG-1998; 98US-0091949P.

PR 10-AUG-1998; 98US-0091959P.

PR 17-AUG-1998; 98US-0091966P.

PR 17-AUG-1998; 98US-0091967P.

PR 17-AUG-1998; 98US-0091968P.

PR 17-AUG-1998; 98US-00919697P.

PR 18-AUG-1998; 98US-0091975P.

PR 18-AUG-1998; 98US-00919759P.

PR 22-MAY-1998; 98US-0097022P.

PR 28-MAY-1998; 98US-0097052P.

PR 28-MAY-1998; 98US-0097054P.

PR 26-AUG-1998; 98US-0097555P.

PR	26-AUG-1998;	98US-0097971P.	Qy	361	HELGIVFNMLHDNSKPCISINGPLSTSRIIVMAPVMAHVDPPEPKSPCSARFITEFLDNGY	420
PR	26-AUG-1998;	98US-0097974P.	Db	361	HELGIVFNMLHDNSKPCISINGPLSTSRIIVMAPVMAHVDPPEPKSPCSARFITEFLDNGY	420
PR	01-SEP-1998;	98US-0098014P.	Qy	421	GHCLIDKPEAPLHLEPTVTPGKDYDADRCOLTFGDSRHCPQLPPPAAIWCSGHNLNGHA	480
PR	01-SEP-1998;	98US-0098716P.	Db	421	GHCLIDKPEAPLHLEPTVTPGKDYDADRCOLTFGDSRHCPQLPPPAAIWCSGHNLNGHA	480
PR	02-SEP-1998;	98US-0098723P.	Qy	481	MCQTKHSPWADGTPCGPAQACMGCRQLHMDQDNPNTPOQGGWPGWPKRDCSRTICGGV	540
PR	02-SEP-1998;	98US-0098803P.	Db	481	MCQTKHSPWADGTPCGPAQACMGCRQLHMDQDNPNTPOQGGWPGWPKRDCSRTICGGV	540
PR	02-SEP-1998;	98US-0098821P.	Qy	541	QFSSRCTRTPRNGSKYCEBRTRRSCTEDCP7GSAALTERBECOAATNHRDTLIFKSF	600
PR	03-SEP-1998;	98US-0098843P.	Db	541	QFSSRCTRTPRNGSKYCEBRTRRSCTEDCP7GSAALTFREREQCAAATNHRDTLIFKSF	600
PR	10-SEP-1998;	98US-0099602P.	Qy	601	PGPMDWVPRITGVAPDQCKLTQCARALGTYVLEPRVVDGTPCSPDSSSYCQSRCIHA	660
PR	10-SEP-1998;	98US-0099741P.	Db	601	PGPMDWVPRITGVAPDQCKLTQCARALGTYVLEPRVVDGTPCSPDSSSYCQSRCIHA	660
PR	10-SEP-1998;	98US-0099754P.	Qy	601	PGPMDWVPRITGVAPDQCKLTQCARALGTYVLEPRVVDGTPCSPDSSSYCQSRCIHA	660
PR	10-SEP-1998;	98US-0099763P.	Db	601	PGPMDWVPRITGVAPDQCKLTQCARALGTYVLEPRVVDGTPCSPDSSSYCQSRCIHA	660
PR	10-SEP-1998;	98US-0099812P.	Qy	721	GRHSIVLALKLPDGSVALNGBYTLMSPTDVLPGVASLRYSGATASETLSGHGGLAQP	780
PR	15-SEP-1998;	98US-0100388P.	Db	721	GRHSIVLALKLPDGSVALNGBYTLMSPTDVLPGVASLRYSGATASETLSGHGGLAQP	780
PR	16-SEP-1998;	98US-0100622P.	Qy	720	GCDRIGSKKKFDKCNVCGGDSGCKQSGSFRKPFYGNVNTTFRAGATHILVRQGNP	720
PR	16-SEP-1998;	98US-0100664P.	Db	661	GCDRIGSKKKFDKCNVCGGDSGCKQSGSFRKPFYGNVNTTFRAGATHILVRQGNP	720
PR	16-SEP-1998;	98US-0100975P.	Qy	601	PGPMDWVPRITGVAPDQCKLTQCARALGTYVLEPRVVDGTPCSPDSSSYCQSRCIHA	660
PR	16-SEP-1998;	98US-0101751P.	Db	661	PGPMDWVPRITGVAPDQCKLTQCARALGTYVLEPRVVDGTPCSPDSSSYCQSRCIHA	660
PR	17-SEP-1998;	98US-0101933P.	Qy	721	GRHSIVLALKLPDGSVALNGBYTLMSPTDVLPGVASLRYSGATASETLSGHGGLAQP	780
PR	17-SEP-1998;	98US-0100981P.	Db	721	GRHSIVLALKLPDGSVALNGBYTLMSPTDVLPGVASLRYSGATASETLSGHGGLAQP	780
PR	17-SEP-1998;	98US-0101062P.	Qy	720	GCDRIGSKKKFDKCNVCGGDSGCKQSGSFRKPFYGNVNTTFRAGATHILVRQGNP	720
PR	18-SEP-1998;	98US-0101068P.	Db	661	GCDRIGSKKKFDKCNVCGGDSGCKQSGSFRKPFYGNVNTTFRAGATHILVRQGNP	720
PR	23-SEP-1998;	98US-0101471P.	Qy	721	GRHSIVLALKLPDGSVALNGBYTLMSPTDVLPGVASLRYSGATASETLSGHGGLAQP	780
PR	23-SEP-1998;	98US-0101472P.	Db	721	GRHSIVLALKLPDGSVALNGBYTLMSPTDVLPGVASLRYSGATASETLSGHGGLAQP	780
PR	23-SEP-1998;	98US-0101475P.	Qy	781	LTLQVLVAGNPDPDTRYSFVPRPPSTPRTPQOWLHRAQILELIRRTPWAGRK	837
PR	23-SEP-1998;	98US-0101477P.	Db	781	LTLQVLVAGNPDPDTRYSFVPRPPSTPRTPQOWLHRAQILELIRRTPWAGRK	837
PR	24-SEP-1998;	98US-0101738P.	Qy	781	LTLQVLVAGNPDPDTRYSFVPRPPSTPRTPQOWLHRAQILELIRRTPWAGRK	837
PR	24-SEP-1998;	98US-0101739P.	Db	781	LTLQVLVAGNPDPDTRYSFVPRPPSTPRTPQOWLHRAQILELIRRTPWAGRK	837
PR	24-SEP-1998;	98US-0101743P.	Qy	RESULT 13		
PR	24-SEP-1998;	98US-0101922P.	Db	ABU84438	ABU84438 standard; protein; 837 AA.	
PR	25-SEP-1998;	98US-0101786P.	Qy	XX	ID ABU84438	
PR	29-SEP-1998;	98US-0102207P.	Db	XX	XX	
PR	29-SEP-1998;	98US-0102240P.	Qy	XX	AC ABU84438;	
PR	29-SEP-1998;	98US-0104330P.	Db	XX	XX	
PR	30-SEP-1998;	98US-0102331P.	Qy	XX	DT 02-AUG-2003 (first entry)	
PR	30-SEP-1998;	98US-0102487P.	Db	XX	XX	
PR	30-SEP-1998;	98US-010570P.	Qy	XX	DE Human secreted/transmembrane protein (PRO) #116.	
PR	30-SEP-1998;	98US-010571P.	Db	XX	XX	
PR	01-OCT-1998;	98US-0102571P.	Qy	XX	DE Human; secreted and transmembrane protein; PRO; TNF-alpha; KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; KW tissue typing.	
PR	01-OCT-1998;	98US-0102684P.	Db	XX	XX	
PR	02-OCT-1998;	98US-0104677P.	Qy	XX	PR 18-SEP-1997; 97US-0059263P.	
PR	06-OCT-1998;	98US-0103965P.	Db	XX	PR 17-OCT-1997; 97US-0059266P.	
PR	06-OCT-1998;	98US-0103258P.	Qy	XX	PR 21-JUN-2002; 2002US-00176756.	
Db	1	MSQTGSHPGGRGLAGRMWQGCPCLLPIPLIVPLSWLWILLASLSPSLPREE	60	PR 28-OCT-1997; 97US-0053541P.		
Db	1	MSQTGSHPGGRGLAGRMWQGCPCLLPIPLIVPLSWLWILLASLSPSLPREE	60	PR 28-OCT-1997; 97US-0053544P.		
Qy	61	IVPPEKLNGSTVPGSGAPARLCLQAFGETLLEQDGSVYEGLTQYLGQAPELLG	120	PR 28-OCT-1997; 97US-0053564P.		
Db	61	IVPPEKLNGSTVPGSGAPARLCLQAFGETLLEQDGSVYEGLTQYLGQAPELLG	120	PR 29-OCT-1997; 97US-0053734P.		
Qy	121	GAEPGTYLGTGTINGDPESVSLHWDGQALLGCVLQYRGAEHLQPLEGGTPNSAGCPGAAHI	180	PR 31-OCT-1997; 97US-006103P.		
Db	121	GAEPGTYLGTGTINGDPESVSLHWDGQALLGCVLQYRGAEHLQPLEGGTPNSAGCPGAAHI	180	PR 31-OCT-1997; 97US-0061103P.		
Qy	181	LRRKSPASGQGPMCNTYKAPLGSSPSPRRAKRFASLSRFTVLLVADDKNAAFHGAGLKR	240	PR 31-OCT-1997; 97US-0061103P.		
Db	181	LRRKSPASGQGPMCNTYKAPLGSSPSPRRAKRFASLSRFTVLLVADDKNAAFHGAGLKR	240	PR 31-OCT-1997; 97US-0061103P.		
Qy	241	YLTNTWAAATAFKHPSIRNPVSLVYTRVLVGSGEEGPQGPAQTLRSFCWQRLN	300	PR 31-OCT-1997; 97US-0061103P.		
Db	241	YLTNTWAAATAFKHPSIRNPVSLVYTRVLVGSGEEGPQGPAQTLRSFCWQRLN	300	PR 31-OCT-1997; 97US-0061103P.		
Qy	301	TPEDSDPBDHDTAILTRQDLCGIVGSTCDTLGMADYGVTCIDPARSCAIVEDDGLOSSFTA	360	PR 21-NOV-1997; 97US-006120P.		
Db	301	TPEDSGDPDHDTAILTRQDLCGIVGSTCDTLGMADYGVTCIDPARSCAIVEDDGLOSSFTA	360	PR 24-NOV-1997; 97US-006166P.		
Qy	301	TPEDSGDPDHDTAILTRQDLCGIVGSTCDTLGMADYGVTCIDPARSCAIVEDDGLOSSFTA	360	PR 24-NOV-1997; 97US-0066772P.		

PR	11-DEC-1997;	97US-0069335P.	PR	19-JUN-1998;	98US-0089952P.
PR	12-DEC-1997;	97US-0069425P.	PR	22-JUN-1998;	98US-009026P.
PR	17-DEC-1997;	97US-0069870P.	PR	22-JUN-1998;	98US-009022P.
PR	18-DEC-1997;	97US-0068017P.	PR	22-JUN-1998;	98US-009024P.
PR	10-MAR-1998;	98US-0077450P.	PR	24-JUN-1998;	98US-009043P.
PR	11-MAR-1998;	98US-0077632P.	PR	24-JUN-1998;	98US-009044P.
PR	11-MAR-1998;	98US-0077649P.	PR	24-JUN-1998;	98US-0090461P.
PR	20-MAR-1998;	98US-0078888P.	PR	24-JUN-1998;	98US-0090535P.
PR	20-MAR-1998;	98US-0078933P.	PR	24-JUN-1998;	98US-0090540P.
PR	27-MAR-1998;	98US-0079664P.	PR	25-JUN-1998;	98US-0090655P.
PR	27-MAR-1998;	98US-0079785P.	PR	25-JUN-1998;	98US-009066P.
PR	31-MAR-1998;	98US-0080107P.	PR	25-JUN-1998;	98US-0090678P.
PR	15-APR-1998;	98US-0080194P.	PR	25-JUN-1998;	98US-0090688P.
PR	01-APR-1998;	98US-0080327P.	PR	25-JUN-1998;	98US-0090690P.
PR	01-APR-1998;	98US-0080333P.	PR	25-JUN-1998;	98US-0090694P.
PR	08-APR-1998;	98US-0081049P.	PR	24-JUN-1998;	98US-0090698P.
PR	08-APR-1998;	98US-0081070P.	PR	01-JUL-1998;	98US-0091154P.
PR	09-APR-1998;	98US-0081193P.	PR	02-JUL-1998;	98US-0091478P.
PR	15-APR-1998;	98US-0080194P.	PR	02-JUL-1998;	98US-0091486P.
PR	21-APR-1998;	98US-0082568P.	PR	02-JUL-1998;	98US-0091636P.
PR	21-APR-1998;	98US-0082569P.	PR	02-JUL-1998;	98US-0091638P.
PR	22-APR-1998;	98US-0082704P.	PR	01-JUL-1998;	98US-0091319P.
PR	22-APR-1998;	98US-0082797P.	PR	01-JUL-1998;	98US-009154P.
PR	28-APR-1998;	98US-0083322P.	PR	02-JUL-1998;	98US-00105413.
PR	29-APR-1998;	98US-0083495P.	PR	02-JUL-1998;	98US-0090862P.
PR	29-APR-1998;	98US-0083496P.	PR	02-JUL-1998;	98US-0090863P.
PR	29-APR-1998;	98US-0083497P.	PR	02-JUL-1998;	98US-0090864P.
PR	29-APR-1998;	98US-0083559P.	PR	02-JUL-1998;	98US-0091010P.
PR	05-MAY-1998;	98US-0084366P.	PR	01-JUL-1998;	98US-009132P.
PR	06-MAY-1998;	98US-0084414P.	PR	02-JUL-1998;	98US-009406P.
PR	07-MAY-1998;	98US-0084463P.	PR	04-AUG-1998;	98US-0095282P.
PR	07-MAY-1998;	98US-0084640P.	PR	10-AUG-1998;	98US-009538P.
PR	07-MAY-1998;	98US-0084643P.	PR	10-AUG-1998;	98US-0096012P.
PR	15-MAY-1998;	98US-0085579P.	PR	17-AUG-1998;	98US-0096757P.
PR	15-MAY-1998;	98US-0085580P.	PR	17-AUG-1998;	98US-0096766P.
PR	15-MAY-1998;	98US-0085581P.	PR	17-AUG-1998;	98US-009687P.
PR	15-MAY-1998;	98US-0085700P.	PR	17-AUG-1998;	98US-0096871P.
PR	18-MAY-1998;	98US-0086023P.	PR	18-AUG-1998;	98US-0096877P.
PR	22-MAY-1998;	98US-0086392P.	PR	18-AUG-1998;	98US-0096949P.
PR	22-MAY-1998;	98US-0086486P.	PR	18-AUG-1998;	98US-0096959P.
PR	28-MAY-1998;	98US-0087098P.	PR	18-AUG-1998;	98US-0097022P.
PR	28-MAY-1998;	98US-0087208P.	PR	26-AUG-1998;	98US-009752P.
PR	02-JUN-1998;	98US-0087609P.	PR	17-AUG-1998;	98US-009754P.
PR	02-JUN-1998;	98US-0087759P.	PR	26-AUG-1998;	98US-009755P.
PR	03-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-0097911P.
PR	04-JUN-1998;	98US-0088025P.	PR	26-AUG-1998;	98US-009794P.
PR	04-JUN-1998;	98US-0088028P.	PR	09-SEP-1998;	98US-0098014P.
PR	05-JUN-1998;	98US-0088029P.	PR	01-SEP-1998;	98US-009816P.
PR	09-JUN-1998;	98US-0088821P.	PR	01-SEP-1998;	98US-009823P.
PR	04-JUN-1998;	98US-00888033P.	PR	02-SEP-1998;	98US-009830P.
PR	10-JUN-1998;	98US-0088832P.	PR	02-SEP-1998;	98US-009831P.
PR	05-JUN-1998;	98US-0088832P.	PR	02-SEP-1998;	98US-009832P.
PR	10-JUN-1998;	98US-0088816P.	PR	15-SEP-1998;	98US-0100388P.
PR	11-JUN-1998;	98US-0088870P.	PR	16-SEP-1998;	98US-010062P.
PR	10-JUN-1998;	98US-0088812P.	PR	16-SEP-1998;	98US-010064P.
PR	05-JUN-1998;	98US-0088811P.	PR	16-SEP-1998;	98US-0100741P.
PR	10-JUN-1998;	98US-0088821P.	PR	16-SEP-1998;	98US-010151P.
PR	10-JUN-1998;	98US-0088865P.	PR	16-SEP-1998;	98US-0099763P.
PR	10-JUN-1998;	98US-00888722P.	PR	10-SEP-1998;	98US-0099830.
PR	11-JUN-1998;	98US-0088873P.	PR	17-SEP-1998;	98US-0101068P.
PR	11-JUN-1998;	98US-0088863P.	PR	17-SEP-1998;	98US-010119P.
PR	11-JUN-1998;	98US-0088811P.	PR	17-SEP-1998;	98US-0100330P.
PR	12-JUN-1998;	98US-0088824P.	PR	18-SEP-1998;	98US-0100349P.
PR	12-JUN-1998;	98US-0088909P.	PR	18-SEP-1998;	98US-010114P.
PR	16-JUN-1998;	98US-00889105P.	PR	18-SEP-1998;	98US-0101668P.
PR	16-JUN-1998;	98US-00889512P.	PR	23-SEP-1998;	98US-010171P.
PR	17-JUN-1998;	98US-00889538P.	PR	23-SEP-1998;	98US-010172P.
PR	17-JUN-1998;	98US-00889538P.	PR	23-SEP-1998;	98US-0101475P.
PR	17-JUN-1998;	98US-0089653P.	PR	23-SEP-1998;	98US-0101477P.
PR	18-JUN-1998;	98US-0089908P.	PR	24-SEP-1998;	98US-0101738P.

PR	24-SEP-1998;	98US-0101739P.	Qy	781	LTLQVLYVAGNPQDTTRLYSFFVPRPTSPTRPTQDYLHRAQILELRRPWAGRK	837
PR	24-SEP-1998;	98US-0101739P.	Db	781	LTLQVLYVAGNPQDTTRLYSFFVPRPTSPTRPTQDYLHRAQILELRRPWAGRK	837
PR	24-SEP-1998;	98US-0101922P.				
PR	29-SEP-1998;	98US-0101786P.				
PR	29-SEP-1998;	98US-0102207P.				
PR	29-SEP-1998;	98US-0102240P.				
PR	29-SEP-1998;	98US-0102330P.				
PR	29-SEP-1998;	98US-0102331P.				
PR	30-SEP-1998;	98US-0102487P.				
PR	30-SEP-1998;	98US-010570P.				
PR	30-SEP-1998;	98US-0102571P.				
PR	01-OCT-1998;	98US-0102684P.				
PR	01-OCT-1998;	98US-0102687P.				
PR	02-OCT-1998;	98US-0102965P.				
PR	06-OCT-1998;	98US-0103250P.				
PR	06-OCT-1998;	98US-0103444P.				
PR	07-OCT-1998;	98US-01168978.				
PR	07-OCT-1998;	98US-01168978.				
Qy	1	MSQTGSHPERGLACRMLNQAGOPCILIPPIVPLSMWLLILLASPLPREEE	Score 4563; DB 6; Length 837;			
Best Local Similarity	99.8%;	Prod. No. 0;	Indels 1;	Gaps 0;		
Matches 836; Conservative	99.9%;	0;	Mismatches 0;			
Db	1	MSQTGSHPERGLACRMLNQAGOPCILIPPIVPLSMWLLILLASPLPREEE	60			
Qy	61	IVFPERKLNGSVLPGSGAPARLICRLQATGETLLEIQLDGSQVVEGTVQYQGAPELIG	120			
Db	61	IVFPERKLNGSVLPGSGAPARLICRLQAFGETLLEIQLDGSQVVEGTVQYQGAPELIG	120			
Qy	121	GAEPGTYLTCTINGDPESTASLHWGGALLGVLQYRGAGELHQLPLEGTPNSAGGPGAAH	180			
Db	121	GAEPGTYLTCTINGDPESTASLHWGGALLGVLQYRGAGELHQLPLEGTPNSAGGPGAAH	180			
Qy	181	LRRKSPASQGPMCNVKAPLGSPSPRPAKRFASLRSRVEVTLVADKMAAFHGAGIKR	240			
Db	181	LRRKSPASQGPMCNVKAPLGSPSPRPAKRFASLRSRVEVTLVADKMAAFHGAGIKR	240			
Qy	241	YLTITMWAATAKAKAFKHPSPINPNSUJYTRVILGSEEEQVQGSPSAACTLRSFCAWORGLN	300			
Db	241	YLTITMWAATAKAKAFKHPSPINPNSUJYTRVILGSEEEQVQGSPAAQTLSRSPCAWORGLN	300			
Qy	301	TPEDSDPDDHDTAILETRDQLCGVSTCDLGMDA9GTYCDPARSACIYEDDGQLOSAFTA	360			
Db	301	TPEDSDPDDHDTAILETRDQLCGVSTCDLGMDA9GTYCDPARSACIYEDDGQLOSAFTA	360			
Qy	361	HELGIVFMILHDNSKPCISLNGPLSTSRHYMAPTAHVDPEPMSPCSARFIDFLDNGY	420			
Db	361	HELGIVFMILHDNSKPCISLNGPLSTSRHYMAPTAHVDPEPMSPCSARFIDFLDNGY	420			
Qy	421	GHCILDKPEA1PHLPVTFPGKDYDADRCOOLTFGPDSSRHCPCQLPQPCALWCSGHLNGA	480			
Db	421	GHCILDKPEA1PHLPVTFPGKDYDADRCOOLTFGPDSSRHCPCQLPQPCALWCSGHLNGA	480			
Qy	481	NCQTKRSPWAQGTPCGPAQACMGCRCLHMDLQDFNIPQAGGGMGPQGDCSRTGCGEV	540			
Db	481	NCQTKRSPWAQGTPCGPAQACMGCRCLHMDLQDFNIPQAGGGMGPQGDCSRTGCGEV	540			
Qy	541	QFSSRDCTRPVRNGKTYCEGRTRPRSCNTEDCPGTSALTFRQQCAAYNHRDLFKSF	600			
Db	541	QFSSRDCTRPVRNGKTYCEGRTRPRSCNTEDCPGTSALTFRQQCAAYNHRDLFKSF	600			
Qy	601	PGEMDKWVPRYTGVAPOQQKUTCQARALGYYVVLBPRVDCTPCSPDSSSSVQGRCRTHA	660			
Db	601	PGEMDKWVPRYTGVAPOQQKUTCQARALGYYVVLBPRVDCTPCSPDSSSSVQGRCRTHA	660			
Qy	661	GCDRTIGSKKKEDKCMYGGDGSGSXQSGSFRKFYXGNNVVT1PAGATHILVRQGNP	720			
Db	661	GCDRTIGSKKKEDKCMYGGDGSGSXQSGSFRKFYXGNNVVT1PAGATHILVRQGNP	720			
Qy	721	GRHSIYLALKLPDGSYALNGEXTLMSPDTPDVYLPGAVSLRYSGATASETLSGHGPLAQ	780			
Db	721	GRHSIYLALKLPDGSYALNGEXTLMSPDTPDVYLPGAVSLRYSGATASETLSGHGPLAQ	780			

Query Match	99.8%	Score 4563;	DB 6;	Length 837;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches	836;	Mismatches 0;	Indels 0;	Gaps 0;
Conservative				
Py				
Py				

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Db	61	IVEPERKINGSVLPVPGSAGAPRLLCRIQAFGETLLEQDGSVQVEGLTVYLGQAPELLG	120
Qy	121	GAEPGTYLTGTINGDPESYASLHWGGALLGVLYRGAEFLHLOPLEGGTGTPNSAGGGFAHI	180
Db	121	GAEPGTYLTGTINGDPESYASLHWGGALLGVLYRGAEFLHLOPLEGGTGTPNSAGGGFAHI	180
Qy	181	LRRKS PASSQGPMCNVKAPLGSPSPRREAKFASLSREVETLTVYADDKNAFAFHAGLKL	240
Db	181	LRRKS PASSQGPMCNVKAPLGSPSPRREAKFASLSREVETLTVYADDKNAFAFHAGLKL	240
Qy	241	YLITTVMAAAKAKFHKPSIARNPVSLLVTRLVLGSEEEGPQVGPQPSAAQTLRSFCANQRLN	300
Db	241	YLITTVMAAAKAKFHKPSIARNPVSLLVTRLVLGSEEEGPQVGPQPSAAQTLRSFCANQRLN	300
Qy	301	TPEPSPDPHDFTDIAFLTRDLCGVSTCDTIGMADYGTCDTIGMADYGTCDTIGMADYGTCD	360
Db	301	TPEPSPDPHDFTDIAFLTRDLCGVSTCDTIGMADYGTCDTIGMADYGTCDTIGMADYGTCD	360
Qy	361	HELGIVFVNMLHDNSPCISLNGPLSTSRYMAPVVAHDPEPWPSPSOSARFTIDFLDNGY	420
Db	361	HELGIVFVNMLHDNSPCISLNGPLSTSRYMAPVVAHDPEPWPSPSOSARFTIDFLDNGY	420
Qy	421	GHCLIDKPEAPLHLPVTPPKSDYDADRCQLTFGPDSRHCPOLPPCAALMCSGHLNHGHA	480
Db	421	GHCLIDKPEAPLHLPVTPPKSDYDADRCQLTFGPDSRHCPOLPPCAALMCSGHLNHGHA	480
Qy	481	MCQTHSPSPWADGTPCPAQACMGGRCLHMDQDFTNIPQAGGWGPNGPWWGDCSRCTCGGGV	540
Db	481	MCQTHSPSPWADGTPCPAQACMGGRCLHMDQDFTNIPQAGGWGPNGPWWGDCSRCTCGGGV	540
Qy	541	QFSSSDCTRPYPRNGSKYCBGRTTRPRSCNTEDCPTCSALTFREEQAAYNERTDLKSF	600
Db	541	QFSSSDCTRPYPRNGSKYCBGRTTRPRSCNTEDCPTCSALTFREEQAAYNERTDLKSF	600
Qy	601	PGPMWVPRYGVAPODQCKLTQARALGTYYLEPRVVDGTPCSPDSSSYCQGRCHHA	660
Db	601	PGPMWVPRYGVAPODQCKLTQARALGTYYLEPRVVDGTPCSPDSSSYCQGRCHHA	660
Qy	661	GCDRTIGSKKKFDKCMVCGDGSCKQSNSPRKFRRYGNNTVTIPAGATHLVRQOQNP	720
Db	661	GCDRTIGSKKKFDKCMVCGDGSCKQSNSPRKFRRYGNNTVTIPAGATHLVRQOQNP	720
Qy	721	GRHSITVALKLUFDGSYALNGENTLIMSPDNTVPGAYSLRYSGATASRTLSCHGPTLAQ	780
Db	721	GRHSITVALKLUFDGSYALNGENTLIMSPDNTVPGAYSLRYSGATASRTLSCHGPTLAQ	780
Qy	781	LTLOQIVVAGNPDTDRYSSFFVPRPTSTPRPTQDWHLRRQIQLTLLRRPWPAGRK	837
Db	781	LTLOQIVVAGNPDTDRYSSFFVPRPTSTPRPTQDWHLRRQIQLTLLRRPWPAGRK	837
RESULT	15		
ID	ABR65702	standard; protein; 837 AA.	
XX	ABR65702;		
XX	05-AUG-2003	(first entry)	
DE	Human secreted polypeptide PRO1563,	SEQ ID NO:352.	
XX			
KW	Human; PRO; secreted protein; transmembrane protein;		
KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;		
KW	chondrocyte; proliferation; differentiation; cartilage disorder;		
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;		
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum;		
KW	liver; drug screening; transgenic animal; genetic analysis;		
KW	antiarthritic; vulnery; gene therapy.		
XX			
OS	Homo sapiens.		
XX			
US2003036159-A1.			

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Search completed: April 1, 2005, 12:48:26
 Job time : 186 secs

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3	4570	100.0	837	4	US-09-122-126B-2	Sequence 2, Appli	Sequence 2, Appli	3 TPEDSDPDHFDTAILFTRDQICGVSTCDTIGMADGVTCDFPARSCLIVEDDCLQSAFTAA 360
4	2158	47.2	950	4	US-09-122-126B-2	Sequence 4, Appli	Sequence 4, Appli	4 YLTVMAAAAKAKPHPSIRNPVSLVTVRLVILGSBEGPOQPSAAQTLRSPCAWQRLN 300
5	2135	46.7	967	4	US-09-122-126B-2	Sequence 2, Appli	Sequence 2, Appli	5 YLTVMAAAAKAKPHPSIRNPVSLVTVRLVILGSBEGPOQPSAAQTLRSPCAWQRLN 300
6	2133	46.6	949	4	US-09-122-126B-2	Sequence 2, Appli	Sequence 2, Appli	6 YLTVMAAAAKAKPHPSIRNPVSLVTVRLVILGSBEGPOQPSAAQTLRSPCAWQRLN 300
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11	1793.5	39.2	608	4	US-09-122-126B-2	Sequence 13, Appli	Sequence 13, Appli	11 YLTVMAAAAKAKPHPSIRNPVSLVTVRLVILGSBEGPOQPSAAQTLRSPCAWQRLN 300
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 1, 2005, 12:21:01 ; Search time 43 Seconds
(without alignments)
1453.053 Million cell updates/sec

Title: US-09-634-287E-2

Perfect score: 4570

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SUMMARIES

RESULT 1
US-09-122-126B-2

; Sequence 2, Appli

; Patent No. 6451575

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Scribb Company

; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES

; FILE REFERENCE: DM6909

; CURRENT APPLICATION NUMBER: US/09/122,126B

; CURRENT FILING DATE: 1998-07-24

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO: 2

; LENGTH: 837

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-122-126B-2

Query Match 100.0%; Score 4570; DB 4; Length 837;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 837; Conservative 0;

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DB 1 MSQTGSHPGRGLAGRWLNGA.....LHRRAQIILBLIRRWRAGRK 837

QY 1 MSQTGSHPGRGLAGRWLNGA.....LHRRAQIILBLIRRWRAGRK 837

ALIGNMENTS

RESULT 2
US-09-122-126B-2

; Sequence 2, Appli

; Patent No. 6451575

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Scribb Company

; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES

; FILE REFERENCE: DM6909

; CURRENT APPLICATION NUMBER: US/09/122,126B

; CURRENT FILING DATE: 1998-07-24

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO: 2

; LENGTH: 837

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-122-126B-2

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Qy	481	MCQTKHSWADGTPCGPQAQCMGCRCLHMDQDQDNIPQAGGWPCKPGDCSRTEGGV	540	Db	361	HELGHFMNLHDNSKFCISLNGPLSTSRSRHYMAPWMBHVDDEPNSPCSAFRITD	420
Db	481	MCQTKHSWADGTPCGPQAQCMGCRCLHMDQDQDNIPQAGGWPCKPGDCSRTEGGV	540	Qy	421	GHCLLDPKPEAPLHLPLVTEPDKDRCQLTFFGDPDRHCPOLPPCAALWCSGHNLGHA	480
Qy	541	QFSSRDCTRPVRNGKRYCEGTRTRFRNTEDCPTCSALTRREEQCAAYNHRDLPKF	600	Db	421	GHCLLDPKPEAPLHLPLVTEPDKDRCQLTFFGDPDRHCPOLPPCAALWCSGHNLGHA	480
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Qy	661	GCDRIIGSKKKFDKCMVCGGDSGCKSKOSGSFPRKFYNNVTTIPAGATHILVRQGNP	720	Db	541	QFSSRDCTRPVRNGKRYCEGTRTRFRNTEDCPTCSALTRREEQCAAYNHRDLPKF	600
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Qy	781	LTLQVLYAGNPQDTRLRYSFVPRPPTSPTRPTQDWMHRRQILELRRPWFAGRK	837	Db	661	GCDRIIGSKKKFDKCMVCGGDSGCKSKOSGSFPRKFYNNVTTIPAGATHILVRQGNP	720
Db	781	LTLQVLYAGNPQDTRLRYSFVPRPPTSPTRPTQDWMHRRQILELRRPWFAGRK	837	Qy	721	GRHSIYLAALKLPDGSYALNGEYTLMPSPDVLPGAYSLRQGATASETLSGHGPLAQ	780
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Qy	781	LTLQVLYAGNPQDTRLRYSFVPRPPTSPTRPTQDWMHRRQILELRRPWFAGRK	837	Qy	781	LTLQVLYAGNPQDTRLRYSFVPRPPTSPTRPTQDWMHRRQILELRRPWFAGRK	837
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; APPLICANT: Bristol-Myers Squibb Company							
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES							
; FILE REFERENCE: DM6109A							
; CURRENT FILING DATE: 2000-08-09							
; NUMBER OF SEQ ID NOS: 21							
; SOFTWARE: PatentIn version 3.0							
; SEQ ID NO: 2							
; LENGTH: 837							
; TYPE: PRF							
; ORGANISM: Homo sapiens							
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Qy	181	LRRKSPASQGPQCMVKAQPLGSPSPRPRAKRFAASLHWGGALLQVLYQGRALH	240	Qy	181	LRRKSPASQGPQCMVKAQPLGSPSPRPRAKRFAASLHWGGALLQVLYQGRALH	240
Db	181	LRRKSPASQGPQCMVKAQPLGSPSPRPRAKRFAASLHWGGALLQVLYQGRALH	240	Db	181	LRRKSPASQGPQCMVKAQPLGSPSPRPRAKRFAASLHWGGALLQVLYQGRALH	240
Qy	241	YLITWAAAKAKAPKIPSIRAPVSLVTRVLYGSSEGPVQPSAACTLRSPCWQGN	300	Qy	241	YLITWAAAKAKAPKIPSIRAPVSLVTRVLYGSSEGPVQPSAACTLRSPCWQGN	300
Db	241	YLITWAAAKAKAPKIPSIRAPVSLVTRVLYGSSEGPVQPSAACTLRSPCWQGN	300	Db	241	YLITWAAAKAKAPKIPSIRAPVSLVTRVLYGSSEGPVQPSAACTLRSPCWQGN	300
Qy	301	TPEDSDDEHDFTAILFTRDLCGVSTCDTLCMADYGTCDPARSAIVEDDGLQSFTA	360	Qy	301	TPEDSDDEHDFTAILFTRDLCGVSTCDTLCMADYGTCDPARSAIVEDDGLQSFTA	360

241 YLTVMAAAKAKFHKPSIRNPVSIIVTRIVILSGSBERGPQVGRSAACTLRSFCAWORGLN 300
 241 YLTVMAAAKAKFHKPSIRNPVSIIVTRIVILSGSBERGPQVGRSAACTLRSFCAWORGLN 300
 301 TPESDPDPFDTAILFTQDLCGYSTCDTLMADVGTCDPARSCAVEDDGLQSAFTAA 360
 301 TPESDPDPFDTAILFTQDLCGYSTCDTLMADVGTCDPARSCAVEDDGLQSAFTAA 360
 361 HELGHVFNLHDNSKPCISLNGPLSTSRHVMAPVMAHYDPEEPWSPCSARFTIDFLONGY 420
 DB 361 HELGHVFNLHDNSKPCISLNGPLSTSRHVMAPVMAHYDPEEPWSPCSARFTIDFLONGY 420
 421 GHCLLDKPAHPLPVTPGKDYDADRCQLTGFDPDSHCKPQLPPCAALWCGHNLNGHA 480
 421 GHCLLDKPAHPLPVTPGKDYDADRCQLTGFDPDSHCKPQLPPCAALWCGHNLNGHA 480
 QY 481 MCQTKHSPWADGTPCGPAQACMGRCIIMDQDLPNTIQAQGNGPQWGDCSRTEGGV 540
 DB 481 MCQTKHSPWADGTPCGPAQACMGRCIIMDQDLPNTIQAQGNGPQWGDCSRTEGGV 540
 541 QFSSRDCTRPVPRNGKTYCEGRTRTRFRSNTEDCPGTSALTRPRBEQCAYNHRTDLPKF 600
 DB 541 QFSSRDCTRPVPRNGKTYCEGRTRTRFRSNTEDCPGTSALTRPRBEQCAYNHRTDLPKF 600
 601 PGPMDDWPRYTGVAQDQCKLTCORALGYYYLEPRVTDGTPCSPDSSSVCYQGRCHTA 660
 DB 601 PGPMDDWPRYTGVAQDQCKLTCORALGYYYLEPRVTDGTPCSPDSSSVCYQGRCHTA 660
 661 GCDRIIGSKKKFDKCMVCGDGSGCSKSKGSFPRKFRYQNNVTTIPAGATHILVRQGNNP 720
 DB 661 GCDRIIGSKKKFDKCMVCGDGSGCSKSKGSFPRKFRYQNNVTTIPAGATHILVRQGNNP 720
 721 GHSIYLAALKLPDGSYALNGEYTLMPSPDVLVLPGAVASLRYSGATAASETLSHGPALQ 780
 DB 721 GHSIYLAALKLPDGSYALNGEYTLMPSPDVLVLPGAVASLRYSGATAASETLSHGPALQ 780
 QY 781 LTQQLVAGNPQDTLRYSFFVPRTPSPTRPQDMLHRAQILETRRPPWAGRK 837
 DB 781 LTQQLVAGNPQDTLRYSFFVPRTPSPTRPQDMLHRAQILETRRPPWAGRK 837
 RESULT 4
 US-09-321-987B-4
 ; Sequence 4, Application US/09321987B
 ; Patent No. 6730820
 ; GENERAL INFORMATION:
 ; APPLICANT: Kimble, Judith E
 ; APPLICANT: Billeloch, Robert H
 ; TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
 ; FILE REFERENCE: 950296.95386
 ; CURRENT APPLICATION NUMBER: US/09/321,387B
 ; CURRENT FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/087,170
 ; PRIOR FILING DATE: 1998-05-29
 ; PRIOR APPLICATION NUMBER: 60/129, 023
 ; PRIOR FILING DATE: 1999-04-13
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4, Andover D.J.
 ; LENGTH: 950
 ; TYPE: PRT
 ; ORGANISM: Murine
 US-09-321-987B-4

Query Match 47.2%; Score 2158; DB 4; Length 950;
 Best Local Similarity 49.4%; Pred. No. 2.9e-15;
 Matches 414; Conservative 135; Mismatches 221; Indels 68; Gaps 16;

QY 37 LLLILLAS-LLPSARLA-SPDREBEVTFPEKLNGVSLPGGAPARLCLR1QAFGETL 92
 DB 18 MLLILLAS-TMILCARGAHGRPTEDDEHVLPSLERA--PGHDSTTTRL-RIDAFGQQL 73
 QY 93 LLELEQDSCVQVEGLTVQYLGQAPELLGCAE-----PGTYLTGTGNDPBPESVSL 142

74 HLLQDPSGLAFDPGFLGTVGRSP---GSEAOLHDPGLAHCFSYSTVNGPGSAAAL 129
 143 HWDGGALLGVLQYRGAEHLHQLPFG----GTP - NSAGPGAHILRKSPASGQP 192
 130 SLCEBG-VRGAFYLGQEEPFIOAPGVATERLAPAVPEBESSARPQFHILRRRGSG-GA 187
 QY 193 MCNV------KAPLJSPSPRPR-----RAKRFASLJSPFETL 223
 DB 188 KCGYMDDETLPLSDSRSPESQNTENQWPVRDPTQDAGKPSGPSSIRKKRFVSSPRYVETM 247
 QY 224 WADDKNAUFGAGLKRVLTYMAAAAKAKFHKPSIRNPVSLVYTRVLGSGEGPQYGP 283
 DB / 248 LVADQSMADFHSGLKHYLLTFSVAARYKHSIRNISLUVVKILVYBQKGPEVTS 307
 QY 284 SAAQTLRSPCAORGQLNTPEDSPDPHDFTAILTRQDLCGVSITCDLGMDAUGSTVCDPAR 343
 DB 308 NAALTLRNFCNWNQKQHNSPSDRDPEHYTAILETRQDLCGSHTCDTLGMDAUGSTVCDPAR 367
 QY 344 SCAIVEDGLQSAFTAAHBLGHVFMLEDNSRCPISINGPLSTSRSRHYMAPVMAHDPPEP 403
 DB 368 SCSYEDGLQAAFTAHBLGHVFMMPHDAAKHCASLNGVTGDS-HLMASMLSSLDHSOP 426
 QY 404 WSPCSARPTIDFDLNGYGHCLLDKPEAHLHPVTFPGKDYDADRCQCOLTFGPDSSRHCPCOL 463
 DB 427 WSPSOMATVTSFLDNGHGBCLMDKPNQIKLPSDLPGLTYDANRQCQTFGBESKHCPCDA 486
 QY 464 PPCCAAWCGSHLNGHACMCTQKHSPIQDFTCPGPAQACMGRCIIMDQDLPNTIPQAGEW 523
 DB 487 ASTCTLWCTGTSQGLLIVCQTKHFPWADGTPCSCBKGKWCVNGKTCMKHFAUTPVHGSW 546
 QY 524 GPGPGWGDGSRTCGGTYQFSSRDCTRPVRNGKTYCEGRTRTRSCNTEDCPGSAFLTR 583
 DB 547 GPGPGWGDGSRTCGGTYQFSSRDCTRPVRNGKTYCEGRTRTRSCNTEDCPNNNGKTR 606
 QY 584 BEQCAATHRHTDLFKSFGPMDVPRVTRGVAPODQCKLTQQAALGTYVBLPRVVDGTP 643
 DB 607 BEQCAARNEFPSKASFGNEPVTWTPKAGVSPDKRCLTCBAKGIGFFVLPQKVVDGTP 666
 QY 644 CSDPSSVYCQGRCIHAGCDRIGSKKKFDKCMVCGDGSGCSKSKGSFPRKFRYQYNNV 703
 DB 667 CSDPSSVYCQGRCIHAGCDRIGSKKKFDKCMVCGDGSGCSKSKGSFPRKFRYQYNNV 726
 QY 704 TIPAGATHILVRQGQNPGRHS--IYLALKLPDGSYALNGEYTLMPSPDVLRGAVSLRY 761
 DB 727 TIPAGATHILVRQGQNPGRHS--IYLALKLPDGSYALNGEYTLMPSPDVLRGAVSLRY 785
 QY 762 SGATAASPTLSGHGPALPDTLQVYAGNPQDTRYSFFVPRPRTPS-TPRTPDQDWL 818
 DB 786 SGSSAALERIRSEFSPLKEPLTQVLYMHALRKPKIKFTYFMKKKTESNAIPFSEWV 843

RESULT 5
 US-09-130-491-2
 ; Sequence 2, Application US/09130491
 ; FILE REFERENCE: 09404/041001
 ; GENERAL INFORMATION:
 ; CURRENT APPLICATION NUMBER: US/09/130, 491
 ; CURRENT FILING DATE: 1998-08-07
 ; EARLIER APPLICATION NUMBER: US 60/058,108
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER APPLICATION NUMBER: US 60/054, 961
 ; EARLIER FILING DATE: 1997-08-06
 ; NUMBER OF SEQ ID NOS: 16
 ; SEQ ID NO 2
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; LENGTH: 967
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-130-491-2

Query Match 46.7%; Score 2135; DB 4; Length 967;
Best Local Similarity 49.5%; Pred. No. 1.6e-152;
Matches 415; Conservative 127; Mismatches 226; Indels 70; Gaps 18;

Qy 37 LLLLLASLLPSRLASLPLREEPVTPPKLNGSVLPSGAPAPLQLQAFGETLIEL 96
Db 36 LLLAAALLAVSDALGRPSSEDELVPELERA --PGHGT-TRL-RHAFDQQLDIEL 89
; LENGTH: 949
; TYPE: PRT
; ORGANISM: human
; SEQ ID NO: 2

Qy 97 EODSGVQVEGLTVYQLQGAPELGGAB ---PGT-----YLTGTGTINGDPEVASHLHWDGCA 148
Db 90 RPDSSFLAPGFTLQNVRGK ---SGSETPPLPETDLAHCYFSGVNGDPSAAALSLCGB- 144
; LENGTH: 949
; SEQ ID NO: 2

Qy 149 LLGVLYQRGAEHLHQPLGGTPNSA-GCPGA-----HILRK----- 184
Db 145 VRGAFYJLGEAYTIQPLPAASERIATAAPGKRPAPLQFHLRLRNROQDVGJGTGWWDDE 204
; LENGTH: 949
; SEQ ID NO: 2

Qy 185 -----SPASQGQPMCNVAKP---LGSPBPR-RAKRFASLSSRFVETLV 224
Db 205 PRPTGKAETDEDEGTGEGDGEDEGTGEGDGEQWSPDQPALGQVQPTGTGSTRKRFVSSHYETML 264
; LENGTH: 949
; SEQ ID NO: 2

Qy 225 VADDKMAAFHAGAISKRYLITWAAAAKFKHPSTRNPVSLVTRVLIGSGEESGPQVGS 284
Db 265 VADQSMAEFHGSGLKHYLTLTFSVAARLYKHPSTRNSVSLVVKILVTHDEQKGPETSN 324
; LENGTH: 949
; SEQ ID NO: 2

Qy 285 AAQTLRSFCAWQGLNTPEDSDPHFTDIALFTRDLCVSTCDLGMADVGTVCDPARS 344
Db 325 AALTJNFCWNQWOKHNPSSDRAEHYDFTLFRDLCGQTCDFLGMADVGTVCDPSSR 384
; LENGTH: 949
; SEQ ID NO: 2

Qy 345 CAIVEDDGQOSAFTAHELGFTVHFMNLDNSKPCITSLNGPLSTSRRHMAPVMAHYDPEEFW 404
Db 385 CSYEDDQGQAATTAEHGTVNMPHMDDAKQACASLNG-VNQOSHMMASLMSNDHSQEW 443
; LENGTH: 949
; SEQ ID NO: 2

Qy 405 SPQSCARFTIDPLDNGYGHCLDKPRAPELHLPPVTFPGKDYDADPQCOLTQGDSRHCPCQLP 464
Db 444 SPQSCAYMTISFLDNGHGECLMDKQPQNPQLPGDLPTGTSYDANRQCOFTGEDSKHCPDA 503
; LENGTH: 949
; SEQ ID NO: 2

Qy 465 PPAALWGSGLHNGHAMCOTHSPWADGTPCGPAQACMGRCLEHMDQLODFNTPQAGGKG 524
Db 504 STCSTLWCTGTSGGVLYCOTKHPFWADGTSGBGKWCINGKCYNTKDTKHFEDTPHGSWKG 563
; LENGTH: 949
; SEQ ID NO: 2

Qy 525 PWDGWGDCSRITCGGGVQFSRSDCTRPRNGGGKCEGERTRFRSNTCNEOPTGSALETFRE 584
Db 564 MWGFWGDCSRITCGGGVQTMRECDNPVPKNGGKCEGKVRVRSNCLECDPDKNGKTFRE 623
; LENGTH: 949
; SEQ ID NO: 2

Qy 585 EOCAYAHRDLD-FKSFGPQMDMVPRYTGVAPODQCKLTCQARALGYYTYLEPRVVDCTP 643
Db 624 EOCAHNEETSKASFGSGPA-VENTPKYAVSPKDRCKLICQAKSITGYYFVFLQPKVVDGTP 682
; LENGTH: 949
; SEQ ID NO: 2

Qy 644 CSPDSSISVCYGRCTHAGCDRTIGSKKEDKCMVCGDGSGCSKQSGSPRKFRYGNVNV 703
Db 683 CSPDSTISVCYQGQCVTKAGKDRIDDSKKEFDKGCVGGNGSTCKKISGTSVTSARKGYHDL 742
; LENGTH: 949
; SEQ ID NO: 2

Qy 704 TIPAGATHILVROQGNGPGRHS--TYLALKLPGDSYALNGEYTLIMSPSTDYVLPGAVSLRY 761
Db 743 TIPGTATNTEVKQNRGSRNNGSFLATIAKADGTYLNGDFTLSTLQDQIMYKGSV-LRY 801
; LENGTH: 949
; SEQ ID NO: 2

Qy 762 SGATAASETLSGHGPIQPLTQVLYVAGNQDFTLRLRYSFPRTPS-TRPRTPQDWL 818
Db 802 SGSSAALENTRRSFPLKEPLTQVLYVAGNQDFTLRLRYSFPRTPS-TRPRTPQDWL 859
; LENGTH: 949
; SEQ ID NO: 2

Query Match 46.6%; Score 2131; DB 4; Length 949;
Best Local Similarity 49.3%; Pred. No. 3.2e-152;
Matches 416; Conservative 121; Mismatches 226; Indels 80; Gaps 18;

Qy 37 LLLLLASLLPSRLASLPLREEPVTPPKLNGSVLPSGAPARLQLQAFGETLIEL 96
Db 18 LLLAAALLAVSDALGRPSSEDELVPELERA --PGHGT-TRL-RHAFDQQLDIEL 71
; LENGTH: 949
; SEQ ID NO: 2

Qy 97 EQDGSVQVEGLTVYQLQGAPELGGAB ---PGT-----YLTGTGTINGDPEVASHLHWDGCA 148
Db 72 RPDSSFLAPGFTLQNVRGK ---SGSETPPLPETDLAHCYFSGVNGDPSAAALSLCGB- 126
; LENGTH: 949
; SEQ ID NO: 2

Qy 149 LLGVLYQRGAEHLHQPLGGTPNSA-GCPGA-----HILRK----- 184
Db 127 VRGAPVLLGEAYFQPLPAASERIATAAPEKPPAPLQFHLLRNRFQGD-VGGTCGVV-- 183
; LENGTH: 949
; SEQ ID NO: 2

Qy 200 LGSPSPR-----RAKRFASLSPR----- 219
Db 184 -DDEBEPRTGKAETDEDEGTGEGDGEAOWSPDQPLQGVQCPQTGTGSRKRFVSSHRY 241
; LENGTH: 949
; SEQ ID NO: 2

Qy 220 VETLVYADDKMAAFHAGAISKRYLITWAAAAKFKPSIRPVSLVTRVLIGSGEEGP 279
Db 242 VETVNLVADTALTRNEFCWNOKEONPPSDRDAEHYDTAFLTRDLCGQTCDFLGMADYGTVC 301
; LENGTH: 949
; SEQ ID NO: 2

Qy 280 QVGPSAAQTLRSFCAWQGLNTPEDSDPHFTDIALFTRDLCVSTCDLGMADYGTVC 339
Db 302 EVTSNVAALTJNFCWNQWOKHNPSSDRAEHYDFTLFRDLCGQTCDFLGMADYGTVC 361
; LENGTH: 949
; SEQ ID NO: 2

Qy 340 DPARSAAVBDGGLOSAFTAHELGFTVHFMNLDNSKPCISLNGPLSTSRRHMAPVMAHYD 399
Db 362 DPSSQSVIEDDGLQAAFTAHELGVFENMHDNSKPCISLNGPLSTSRRHMAPVMAHYD 420
; LENGTH: 949
; SEQ ID NO: 2

Qy 400 PEEPNWSPCSARFITTDLNGYGHCLDKPRAPELHLPPVTFPGKDYDADQCOLTQGDSR 459
Db 421 HSQWPWPCSAVMTISLWCTGTSGGVLYCOTKHPFWADGTSGBGKWCINGKCYNTKDTKHFEDTPHGSWKG 480
; LENGTH: 949
; SEQ ID NO: 2

Qy 460 CPOLPPPCAAIWCSGHNGHAMCOTHSPWADGTPCGPAQACMGRCLEHMDQLODFNTPQDWL 519
Db 481 CPDAASSTCSTLWCTGTSGGVLYCOTKHPFWADGTSCEGKWCINGKCYNTKDTKHFEDTPHGSWKG 540
; LENGTH: 949
; SEQ ID NO: 2

Qy 520 AGGWGPWGPNGDGSRITCGGGVQFSRSDCTRPRNGSKYCBERRTRFRPSCTNDTGPQSA 579
Db 541 HGSWGPWGPNGDGSRITCGGGVQFSRSDCTRPRNGSKYCBERRTRFRPSCTNDTGPQSA 600
; LENGTH: 949
; SEQ ID NO: 2

Qy 580 LTERFEOCAATNHRRTDL-FKSFGPQMDMVPRYTGVAPODQCKLTCQARALGYYVLPFRV 638
Db 601 KTFREOCEAINEFSAFSGPAA-VENTPKYAVSPKDRCKLICQAKSITGYYFVFLQPKV 659
; LENGTH: 949
; SEQ ID NO: 2

Qy 639 YNNVVTIPAGATHILVROQGNGPGRHS--TYLALKLPGDSYALNGEYTLIMSPSTDYVLPGAVSLRY 756
Db 720 YHDITIPTGATNTEVKQNRGSRNNGSFLATIAKADGTYLNGDFTLSTLQDQIMYKGSV 779
; LENGTH: 949
; SEQ ID NO: 2

Qy 757 VSLRYSGATAASETLSGHGPIQPLTQVLYVAGNQDFTLRLRYSFPRTPS-TRPRTPQ 815
Db 780 V-LRYSGSAALERTRRSFPLKEPLTQVLYVAGNQDFTLRLRYSFPRTPS-TRPRTPQ 838
; LENGTH: 949
; SEQ ID NO: 2

RESULT 6
US-09-558-559-2

Sequence 2, Application US/09566559
Patent No. 649377
GENERAL INFORMATION:
APPLICANT: Klonowski, Paul
APPLICANT: Allard, John
APPLICANT: Heller, Renu
APPLICANT: Van Ware, Harold
TITLE OF INVENTION: Human Aggrecanase and Nucleic Acid
TUTORIAL INFORMATION:
APPLICANT: V-FKKKKKEESFPLKEPLTQVLYVAGNQDFTLRLRYSFPRTPS-TRPRTPQ 815
APPLICANT: V-LRYSGSAALERTRRSFPLKEPLTQVLYVAGNQDFTLRLRYSFPRTPS-TRPRTPQ 838

Qy 816 DWL 818
 Db 839 ANV 841

RESULT 7
 US-09-445-023A-1
 ; sequence 1, Application US/09445023A
 ; Patent No. 6565858
 ; GENERAL INFORMATION:
 ; APPLICANT: Hirose, Kunitaka
 ; APPLICANT: Inoguchi, Biji
 ; APPLICANT: Hakozaiki, Michinori
 ; APPLICANT: Ishioka, Keiko
 ; APPLICANT: Matsushima, Kouji
 ; APPLICANT: Kuno, Kouji
 ; APPLICANT: Ishida, Yukako
 ; APPLICANT: Kuno, Kouji
 ; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical composition and method of immunologically analyzing human ADAMTS
 ; FILE REFERENCE: Q57092
 ; CURRENT APPLICATION NUMBER: US/09/445, 023A
 ; CURRENT FILING DATE: 1999-12-03
 ; PRIORITY APPLICATION NUMBER: JP 9-160422
 ; PRIORITY FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 14
 ; SEQ ID NO 1: US-09-445-023A-1
 ; SOFTWARE: Patentin version 3.0
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

Query Match 43.7%; Score 1998.5; DB 4; Length 727;
 Best Local Similarity 57.5%; Pred. No. 2.2e-142; Mismatches 105; Indels 7; Gaps 6;
 Matches 353; Conservative 149;

Qy 209 RAKRFAISLRFVETLVVADKMAAFPGAGLKRYLITMAAAAKAKFHKPSIRNPVSLVYTR 268
 Db 9 RCKRFEVSSPRYVETMLVADQSMALFRRGSGKLHYLLTFLSVAARLYKHPKIRNSVSLVYK 68

Qy 269 LVLIGSGPBGPQVPSAAQTLRSFCAVQRGLNTPEDSDPHDPTDFTLFLGCVSTCD 328
 Db 69 ILVYHDBQGPVETSNAALTLRNFCNQWQKQHNPSPDRDAEHYDTAILFTQLCGSOTCD 128

Qy 329 TIGMADGTVCDCPDRSCVIEDDGLQSAFTAHELGHVFLHNDNSPCTCISNGPUSTR 388
 Db 129 TIGMADGTVCDCPDRSCSVEIDDGLQAAFTTAHELGHVFLHNDNSPCTCISNGPUSTR 387

Qy 389 HMAPYMAHVDPEPWSPCSARFIDFLDNGYGHCLLDKPEAPLHLPPVTPGKDYADRQ 448
 Db 188 HMMASMLSNLDSQWPWSPCSAATMITSFLDNGHECLMDKPKQNPQIOLPGDLPSTLYDANRQ 247

Qy 449 CQTFGPPDRHCPQLPQQCAALWCGSHLNGHAMCQTHSPWADGTPCGPAQACMGRCLH 508
 Db 248 CQTFGEDSKHCBDAASTCSTLWCTGTSGGVLVCQTHFPPWADGTSCEGKCTINGKCVN 307

Qy 509 MDOQDFNIPQAGCWPQPGPWGDCSRTICGGTQFSRSDCTREVPRNGKXCEGRTRFRS 568
 Db 308 KTDKRPHDTPFPGSWGPWGBCSRTICGGTQYTMRCBDDNVPKQNGKXCEGRTRFRS 367

Qy 569 CNTEDCPNGSALTFRREEQCAAATNRTDL-PKSFPGPMDWVPRYTGVAQDQCKLTQCARA 627
 Db 368 CNLEDCPNGKTFREEQCEALNEFSTASFGSCPA-NEWIPKXAGVSPKDRKLICQAKG 426

Qy 628 LGYYVLDPRVVDGTPCSDSSVYCOGRCTHAGCDRLIGTSKFKPDICMVCGDGSSCSK 687
 Db 427 IGYPFLQPKVUDGTPCSPDSTSVCQCVKAGCDRILDSKKFDKGVCGGNGSTCK 486

Qy 688 OSSEFRKFRYGNVNNVVTIPAGATHILYRQGNGPHRS--IYIALKLDPGSTALNGETLM 745
 Db 487 IGSVTSVAKPGYHDIVITPTGATNIEVQRORGSRNSRNGSFLAIKAADGTVLNGDYL 546

Qy 746 PSPTDVVLPGAVSILRYSGATASETLSGHGPLAQPLTLQVLVAGNPQDTRLBYSFYVPRP 805
 Db 547 TLEQDINMKGVV-LRGSSAALETRSFSPKEPFTIQVNLARPKCYTFYCKK 605

Qy 806 TPS-TPPTPQDML 818
 Db 606 KESFNAAIPPTESAWV 619

RESULT 8
 US-09-445-023A-12
 ; Sequence 12, Application US/09445023A
 ; Patent No. 6565858
 ; GENERAL INFORMATION:
 ; APPLICANT: Hirose, Kunitaka
 ; APPLICANT: Inoguchi, Biji
 ; APPLICANT: Hakozaiki, Michinori
 ; APPLICANT: Ishioka, Keiko
 ; APPLICANT: Matsushima, Kouji
 ; APPLICANT: Kuno, Kouji
 ; TITLE OF INVENTION: Human ADAMTS-1 protein, gene encoding the same, pharmaceutical composition and method of immunologically analyzing human ADAMTS
 ; FILE REFERENCE: Q57092
 ; CURRENT APPLICATION NUMBER: US/09/445, 023A
 ; CURRENT FILING DATE: 1999-12-03
 ; PRIORITY APPLICATION NUMBER: JP 9-160422
 ; PRIORITY FILING DATE: 1997-06-03
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 727
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 ; US-09-445-023A-12

Query Match 43.5%; Score 1986; DB 4; Length 727;
 Best Local Similarity 56.1%; Pred. No. 2e-141; Mismatches 155; Indels 6; Gaps 5;
 Matches 348; Conservative 111; Mimatches 111; Mimatches 155; Indels 6; Gaps 5;

Qy 203 PS-PRPRRAKRFASLRFVETLVVADKMAAFPGAGLKRYLITMAAAAKAKFHKPSIRNP 261
 Db 2 PSGGPSIRKRCRREVSPRVTMLVADQSMADFHGSGLKHYLLTFLSVAARFYKHPKPSIRNS 61

Qy 262 VSLUVTRVILGSGEGPQVGSAAQTLSFCAWQRGLINTPDDSPDHFDTAILFTQDL 321
 Db 62 ISLUVVKILVYIEEQKGPVETSNAALTLRNFTSWQOHNSPDRDPEHYDTAILFTQDL 121

Qy 322 CGVSTCDTGLADGVGTCDPDRSCVAYEDDGLQSOAFTAHELGHVFLHNDNSKPCISLN 381
 Db 122 CCGTCDTGLADGVGTCDPDRSCVAYEDDGLQSOAFTAHELGHVFLHNDNSKPCISLN 381

Qy 382 GPLSTSRRHMAVPMAYDPEEWSPCSARFIDFLDNGYGHCLLDKPEAPLHLPPVTPGK 441
 Db 182 G-VSGDHLMSMLSSLDHSQWPWSPCSAATMITSFLDNGHECLMDKQNPQPLKSLPQGT 240

Qy 442 DYDADRCQQLTGFPSDRHCPDSSRHCQLPPPCAALWCGSHLNGHAMCQTHSPWADGTPCQAC 501
 Db 241 LYDANRQCOQFIFGEBSRHCPCDAASTCTTLWCTGTSGLLIVCOTKHPFWADGTSCEGKWC 300

Qy 502 MGGRCLHMDQLODQFNIPQAGCWPQPGPWGDCSRTICGGVQFSRSDCTRVPRNGKXCEGRTRFRS 561
 Db 301 VSGKCVNKTDMKHFATVHGSQGPWGPWGDCERTCGGCVQYTMRCBDDNVPKNGKXCEGRTRFRS 360

Qy 562 RTRFRSCNTEDCPGTSALTFRREEQCAAATNRTDLFKSFPGMDWVPRYTGVAQDQCKL 621
 Db 361 KRVYRSCNIECDPDDNGKTPREOCAHNERSKSAFGNEPTVETWPKYGVSPKDRCKL 420

Qy 622 TQARALGYYVLEPRVVDGTPCSDSSVYCOGRCTHAGCDRLIGTSKFKPDICMVCGDGSSCSK 681
 Db 421 TCEAKGIGYFFVFLQPKVUDGTPCSPDSTSVCQCVKAGCDRILDSKKFDKGVCGGNGSTCK 480

Qy 682 GSGCSKISQGSFRKFRYGNVNNVVTIPAGATHILYRQGNGPHRS--IYIALKLDPGSTALNGDYL 739

481 G3TCKNSGIVTSTRPGYHDIVTIPAGATINLEVKHNORGSRNNNSFLAATADGTYILN 540
 Db 481 G3TCKNSGIVTSTRPGYHDIVTIPAGATINLEVKHNORGSRNNNSFLAATADGTYILN 540
 Qy 740 GRYTLMPSPTDVLPGAVSLRYSGATASETLISGHGPPLAQAPATLQVLAQNPQDPLRLYS 799
 Db 541 GNPFLSTLSEQDLTYKGTV-LRYSGSSAALERIERSFSPLKEPTIQLVMGHALRPKIKFT 599
 Qy 800 FFYPRPRTPS-TPRPTPQDWL 818
 Db 600 YFMKCKCTESFNAIPTFSEMW 619

RESULT 9
 US-10-009-332-1
 Sequence 1, Application US/10009332
 Patent No. 6716613
 GENERAL INFORMATION:
 APPLICANT: Kazu DNA Research Institute
 TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING AGGREGANASE ACTIVITY
 FILE REFERENCE: Q6/541
 CURRENT APPLICATION NUMBER: US/10/009-332
 CURRENT FILING DATE: 2001-12-10
 PRIOR APPLICATION NUMBER: JPA Hei 11-321740
 PRIOR FILING DATE: 1999-11-11
 NUMBER OF SEQ ID NOS: 35
 SOFTWARE: PatentIn version 3.1.
 SEQ ID NO 1
 LENGTH: 950
 TYPE: PR
 ORGANISM: Homo sapiens
 US-10-009-332-1

Query Match 41.9%; Score 1917; DB 4; Length 950;
 Best Local Similarity 46.3%; Pred. No. 4.5e-136; Mismatches 267; Indels 52; Gaps 16;
 Matches 31; Conservative 123; Mismatches 267; Indels 52; Gaps 16;

Db 1 MLLGILTLTAAFLQAGTGGFPEPEVYVPLDPLINGRYYWRQGQFQITAF 60
 Qy 37 LLLILLASLPSLARASLPFPREBIVFPEKLGSVU----PGSAPARLICRLQAF 88
 Db 1 QEDFYLHLTDAQFLAPASTEHGVPLQGLTGSSSLRRCFSGDYNALPEPDSFAAVLIC 120
 Qy 89 GETLILLEBDGSGVQEGLPQVYQJQAPPLLGAEP----GTYLTTGTDGPEVASLHD 145
 Db 61 QEDFYLHLTDAQFLAPASTEHGVPLQGLTGSSSLRRCFSGDYNALPEPDSFAAVLIC 120
 Qy 146 GGATIGVLYQRGAEHLHQLPLEGGTENSA--GGPGAHILRK---SPASQGGMCNV-- 196
 Db 120 WNPAILRALDPYKPRAGFESRERRSRRAKREVSIPLNAPAAORNSQGAHILLRGVPG 179
 Qy 197 -----KAPLGSPSPRPR--RAKREASLSSFVETLVVADKMAAHPGAGIK 239
 Db 180 WNPAILRALDPYKPRAGFESRERRSRRAKREVSIPLNAPAAORNSQGAHILLRGVPG 179
 Qy 240 RYLTJVMMAAAAKAFKHPSTRPVSLVTRVILGSGEEQPGVPSAAQTLRSPCAWQRL 299
 Db 240 HYLLTILAAARLYRHPSTLPNPIVIVVVKWLLIDRDSGFKVTEAALTIRNFCAWQRL 299
 Qy 300 NTPEDSPDPPHFDTAAITFTRDLCGCVSTCDTLMADYGTCDPAPSCATYDDGEQSAFTA 359
 Db 300 NKVSDKXHPPEWDTAILFTRDLCGATTCDTLMADVGMCDPKRSCSVIEDGLPSAFT 359
 Qy 360 AHELGHVFMNLDNSKPCISUNGPLSTSRYMAPWMAHDTPEEPWSPCSPARFITDFDNG 419
 Db 360 AHELGHVFMNLDNSKPCISUNGPLSTSRYMAPWMAHDTPEEPWSPCSPARFITDFDNG 419
 Qy 420 YGHCLLDKPEAPLHHPVTFCKDYDADRCQCOLTGFPSDHSRHCQPLPPPCALWCSGHLNGH 479
 Db 419 HGDCLLIDQPSKRPISLPEDLPGASYLTSQOCELAFGVGSRECPYMQYCTKLWCTGKARSG 477
 Qy 480 AMCQTKXHPPEWDTAILFTRDLCGATTCDTLMADVGMCDPKRSCSVIEDGLPSAFT 539

478 MYCQTHFEPWADGTSCEGKICLKGACVERHNLNKHVRD--GSWAKWDPYGPCCSRCTCGGG 535
 Db 478 MYCQTHFEPWADGTSCEGKICLKGACVERHNLNKHVRD--GSWAKWDPYGPCCSRCTCGGG 535
 Qy 540 VQFSRSDCTREPVPRNGKGYCEGRTRTRFSCTNTEDCP-TGSALTBEQCA--YHRTD 595
 Db 536 VQLARQCTNTPTANGKCYCEGRTRTRFSCTNTEDCP-TGSALTBEQCAEFGYNHSTN 595
 Qy 596 LPKSPGPMDWPRYTGVAPODOCKLTCQARALGTYVLEPRYVDTCPSCPDSSYCVQG 655
 Db 596 RLTL--AVATVPKYSGSPADKCKLICRANGTGTYVLAFKVVDTLCSDSTSCVQG 652
 Qy 656 RC1HAGCDRIGSKKRFDKCMVCGGSGCSXQSGSFRKFRGYNNVVTIPAGATHILVR 715
 Db 653 KCIKAGCDDGNLGSCKEDKCGVCGGNNKNSCKVTKGIFTKPMHNGYNVTVAPAGASSDIR 712
 Qy 716 QOGNPG--HRSSTYLAFLKLPDGSYVALNGEYTIMPSPTDVLDVVKGSL-IRYSGTGTAVESLQA 773
 Db 713 QRGYKGJLGDNYNLAJXNSQGKYLQNGHFTVSAVERDLVVKGSL-IRYSGTGTAVESLQA 771
 Qy 774 HGPLAQPLTQLQVLYVAGNPNQDTRLYSFFVPRPTSPSPRPTPD 816
 Db 772 SRPILPPTVETLVSQMTPPVRYSPYTLKPEPREDKSHPKD 814
 RESULT 10
 US-09-369-364A-9
 Sequence 9, Application US/09369364A
 Patent No. 6391610
 GENERAL INFORMATION:
 APPLICANT: Ape, Suneel
 APPLICANT: Hurskainen, Taina L.
 APPLICANT: Hirohata, Satoshi
 TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
 FILE REFERENCE: 26473/4007/10-30-00
 CURRENT APPLICATION NUMBER: US/09/369_364A
 CURRENT FILING DATE: 1999-08-06
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 9
 TYPE: PPT
 ORGANISM: Mus musculus ADAMTS-8
 US-09-369-364A-9

Query Match 39.9%; Score 1824; DB 3; Length 905;
 Best Local Similarity 44.2%; Pred. No. 4.5e-129; Mismatches 23; Indels 104; Gaps 26;
 Matches 373; Conservative 134; Mismatches 23;
 Db 36 WLLLILLASLPSLARASPLP----REBETVPEKLGSVLPGSGAPARLICRLQAF 88
 Qy 10 WPPPLLULQLPPPLVCGAPAGPGTGAQASELUVTPRLPGSA----SELAFLISAF 62
 Qy 89 GETLILLEBDGSGVQEGLPQVYQJQAPPLLGAEP----GTYLTTGTDGPEVASLHD- 143
 Db 63 GQGTVLRLAPDASFLAPEFKIERLGSSAAAGG-EPGLRGCFSGTGVNGERESTAAMSCV 121
 Qy 144 -WPGGALIGVLYQRGAEHLHQLPSEG----TPN--SAGGGAHILRKRSPP---- 186
 Db 122 AGNSGFLA----GEEFTIQQGAGGSDQPHRLQWRGPGQ--RREPDGLAAYFP 173
 Qy 187 -----ASQG----
 Db 174 LPOQLEWEYEMGNGQOERSNDEEDKKDQKGILKETEDSRKVPPFGSKT--RSKRF 229
 Qy 214 ASLSRPFVETLVVADMRMANFHGACLKRYLITWAAKAKHSDVPSLNVTRIVLIG 273
 Db 230 VSEARFETVLLVADMSMAAFYGTDLQNLHNTVMSMAMARLYKHSFSRNSYNLVYKVLTVE 289
 Qy 274 SGEGPQVGPSSAAOTLRSFGAOWQGLNTPEDSDDDHFTDAILFTRDQLGCV-STCDTLM 332
 Db 290 KERNGPEVSDNGGILRNVCWSQRRNPKNSRDPHDFHYDTAILETRQNFGKGEOQDTLM 349
 Qy 333 ADYGTVCDDPARDSCATIYEDDGLQSAFTAHHGLYVFMNLHDNSKPCISUNGPLSTSRRHVM 392

350 ADVGTICDPDKSCSVIKDEGLOAAYTLAHELGHVLSMPHDDSKPCKVYRLFGPMG - KYHMMMA 408
 Db Qy 449 COLTFGDPSRHCOPQLPPCAALWCSGHNLGHAMCQTHSPWADGTPCGPAQACMGGRCGLH 508
 Qy 393 PYMAHYDPEEPWSPCSARFIRTFDLDNGYGHCLIDKPPAFLHLPVTFGKD - YDADRCO 450
 Db 409 PFFIHVNKTLPWSPCSAVYLTELDGHDGCLIDADPTSVLPLPTGPHSTYELDQCK 468
 Db Qy 451 LTFGPDPSRHC - QLPPPCAAWCNSGHING - HAMCQTKHSP - - WADGTPCGPAQACMGG 505
 Db 469 QIFGPDPRHCPTNSVEDCQVL - CARHRSDESPICHTKNSLWADTPCGFHGLCLDGS 527
 Qy 506 CLHMDLQDFNIPQAGGMWPGWPGDOSRITCGGGVQFSSRDCTRPRNGKCYCEGRTR 565
 Db 528 CVLKEDVNPKAVIDGWMWPGWPGCOSRITCGGQIQSNRECDNPMFQNGRFCLGERVK 587
 Qy 566 FRSCNTEDCPTOSALTRBEEQCA -- AYNHRTDLFKSFPGPMWDWPRYTGAQPDQCKLT 622
 Db 588 YOSCNTEBPP-NGKSFREQQCEKYNAYNH-TDLDGMP - - LQWVPAKSYGSPDRCKLF 642
 Qy 623 COARALGXXYYLLEPRVUDGTPCSPDSSVYQGRCTHAGCDRIGSRRKKFOKCMVCGGDD 682
 Db 643 CHARGRSEKPKVEAKVQDGLCPTDUSIVRGQCYRAGCDHVNSPRKLDRCGVCGKG 702
 Qy 683 SGCSKQSGSFKFRGYGNNVVTIPIAGATHILVRQGPNPHRS - - YIALKLPDGSYALNG 740
 Db 703 TACRKLISGTFPSYGNNDIVTIPIAGATNDYTKQRSHGPVRNDGSYALKTANGQYLNG 762
 Qy 741 BYTLMPSPDTVVLPGAWSLRYSGATAASETLSGHGPLAQPLTLQVL-VAGNQDFTLRYS 799
 Db 763 NLAISALEQDILVKGTI-LKYSGSMATLERLQSFOALPEPLTVQLLTVSGEVFPKRYT 821
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RESULT 13
US 09-122-126B-15
; Sequence 15 ; Application US/09122126B
; Patent No. 6515175
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6109
; CURRENT APPLICATION NUMBER: US/09-122-126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 930
; TYPE: PRTE
; ORGANISM: Homo sapiens
; US-09-122-126B-15

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Matches 325; Conservative 120; Mismatches 258; Indels 85; Gaps 19;

Query 87 ARGETLLEQDQEVQEGLTQVQLQAPELLGAEP---GTYLTGTGTDPESYAS 141
Qy 93 AGGRFLFLDIERDGSVIAF-----VPGAGTTSAPTRHRSFCYRGTVDASPRSLAV 145
Db 142 LHWDDGGALLQVQLQTRGAELNQPLREGG----- 168
Qy 146 FDLCCG-LDGFPAVKHARTLKLPLRGPNAEEKGRVYEDGSARILHYTREGFSFEALP 204
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RESULT 14
US-09-634-286A-15
; Sequence 15 ; Application US/09634286A
; Patent No. 6521436
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909A
; CURRENT APPLICATION NUMBER: US/09-634-286A
; CURRENT FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 930
; TYPE: PRTE
; ORGANISM: Homo sapiens
; US-09-634-286A-15

Query Match 34.1%; Score 1558; DB 4; Length 930;
Matches 325; Conservative 120; Mismatches 258; Indels 85; Gaps 19;

Query 87 ARGETLLEQDQEVQEGLTQVQLQAPELLGAEP---GTYLTGTGTDPESYAS 141
Qy 93 AGGRFLFLDIERDGSVIAF-----VPGAGTTSAPTRHRSFCYRGTVDASPRSLAV 145
Db 142 LHWDDGGALLQVQLQTRGAELNQPLREGG----- 168
Qy 146 FDLCCG-LDGFPAVKHARTLKLPLRGPNAEEKGRVYEDGSARILHYTREGFSFEALP 204
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Qy

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		Mismatches	258;
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169	--TPNSAGCPGAHILRRKSPA---SGQGPMC---NVKAPLGSPSPRP--RRA	210	
205	PRASCTP- ASTPEAH - EHAPASNSPNSGRAALASQLDOSALSPAGGSPQTTWRR	259	
211	KRPASLSRFEVETLVVADDKMAAFAHAGAGLKRYLITMAAAFAKFKHSIRNPVSLVTRLV	270	
260	BRSPSARQEVLLVADASMARLYQGLUQHLYTTLASIANLYSHASIEENLIRLAVKVV	319	
271	ILGSGEBGPQVCPSPAACTLRSFCAWGLNTPEDSDPDHFDTAILFTDOLCGVSTCDTL	330	
320	VLGDOKSLEISKNAATTLKNFKWCKWQHONQJDDBEHYDAILFTDOLCGHHSCTDL	379	
331	GMADVCYTCDPARSCLIVEDDQLQSAFTA AHELGIVENMLNDNSKPCISLNGPLSTSRRH	390	
380	GMADVCYTCSPERSCAVIEDDGLIHAFTVAHEIGHLGLSHDDSKFCCEETRGSTEDKR-L	438	
391	NAPVMVAHVDPEEPWSPSARFPTDOLDGXHCLLDEKPEAPLHLPLVTPFGKDYDAHQCQ	450	
439	MSSLTISDASRKPWSKCTSATITFEDGHNCLLDPKLGPEELPQTYDADQCN	498	
451	LTFGDPDSRHCPOLPPPCAALMCSGHLNGHACMOTKHSPPWADGTPCPBAQACMGRCLHMD	510	
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511	QLODFNIPQAGGWGPQPGWGSRTCGGVQPSRSDTTRPFRNGKCYCEGRTRPRSCN	570	
558	KKKKYKSTSSHNGWSGNSWGSQCSRSCGGVQPAVRHNNPAPRNNGRYCTGKRAIYRSC	617	
571	TEDCPGTSALTFREBOCAAYN-HRTDL - FKSFPGPMDWVPRYTGYAPODOCKLTCAORA	627	
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628	LGYYXXLEPRVYDGTPCSPDSSVCYGRCIHAAGCDRIGSKKEDKCMVGGDGSGCSK	687	
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688	QGSFTRKFRXGNNVVTIAPAGATHLVRQ--QGNPGRHSITYALKDGFALNGETLM	745	
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746	PSPTDGVLPGAVSLRSGATASSETLSGHGPLA--QPLTLVOLVAGNPNQDTRLRYFFVP	803	
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Db	451 LTFGDPDSRHCPOLPPPCAALMCSGHLNGHACMOTKHSPPWADGTPCPBAQACMGRCLHMD	510	
Qy	451 LTFGDPDSRHCPOLPPPCAALMCSGHLNGHACMOTKHSPPWADGTPCPBAQACMGRCLHMD	510	
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Qy	511 QLODFNIPQAGGWGPQPGWGSRTCGGVQPSRSDTTRPFRNGKCYCEGRTRPRSCN	570	
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Qy	558 KKKKYKSTSSHNGWSGNSWGSQCSRSCGGVQPAVRHNNPAPRNNGRYCTGKRAIYRSC	617	
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Qy	571 TEDCPGTSALTFREBOCAAYN-HRTDL - FKSFPGPMDWVPRYTGYAPODOCKLTCAORA	627	
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Db	628 LGYYXXLEPRVYDGTPCSPDSSVCYGRCIHAAGCDRIGSKKEDKCMVGGDGSGCSK	687	
Qy	628 LGYYXXLEPRVYDGTPCSPDSSVCYGRCIHAAGCDRIGSKKEDKCMVGGDGSGCSK	687	
Db	674 TGYYVVFSPKVTDGTECRPYSNSVCRGKCVRTGCDGIGSKLOYDKCGVGGDNSSCTK	733	
Qy	674 TGYYVVFSPKVTDGTECRPYSNSVCRGKCVRTGCDGIGSKLOYDKCGVGGDNSSCTK	733	
Db	688 QGSFTRKFRXGNNVVTIAPAGATHLVRQ--QGNPGRHSITYALKDGFALNGETLM	745	
Qy	688 QGSFTRKFRXGNNVVTIAPAGATHLVRQ--QGNPGRHSITYALKDGFALNGETLM	745	
Db	734 IVGTEENKSKSGYTDVRIPEGATHIKYRQFKADQTRFTAYIALLKKNGEYLINGKYMIS	793	
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Db	746 PSPTDGVLPGAVSLRSGATASSETLSGHGPLA--QPLTLVOLVAGNPNQDTRLRYFFVP	803	
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Db	853 K-KSTPK	858	
Qy	853 K-KSTPK	858	
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Db	853 K-KSTPK	858	

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1882.706 Million cell updates/sec						
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Searched: 1413372 seqs, 33152847 residues						
Processing: Minimum Match 0% Maximum Match 100% Listing First 45 Summaries						
Database : Published Applications AA:*						
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2	4570	100.0	837	16	US-10-408-665A-1348	Sequence 1348, Ap
3	4567	100.0	837	16	US-10-628-432-1	Sequence 1, Appli
4	4567	99.9	846	16	US-10-628-32-29	Sequence 29, Appli
5	4566	99.9	837	15	US-10-358-983-11	Sequence 11, Appli
6	4563	99.8	837	15	US-09-446-374-317	Sequence 317, Appli
7	4563	99.8	837	13	US-10-052-86-352	Sequence 352, Appli
8	4563	99.8	837	14	US-10-174-590-352	Sequence 352, Appli
9	4563	99.8	837	14	US-10-176-58-352	Sequence 352, Appli
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11	4563	99.8	837	14	US-10-174-581-352	Sequence 352, Appli
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45	4563	99.8	837	14	US-10-174-576-352	Sequence 352, Appli
ALIGNMENTS						
RESULT 1						
US-10-247-685-2						
; Sequence 2, Application US/10247685						
; Publication No. US20030108998A1						
; GENERAL INFORMATION:						
; APPLICANT: Bristol-Myers Squibb Company						
; TITLE OF INVENTION: AGGREGAN DEGRADING METALLO PROTEASES						
; FILE REFERENCE: DM6905						
; CURRENT APPLICATION NUMBER: US/10/247,685						
; CURRENT FILING DATE: 2002-09-19						
; NUMBER OF SEQ ID NOS: 21						
; SOFTWARE: Patentin version 3.0						
SEQ ID NO: 2						
; LENGTH: 837						
; TYPE: PRT						
; ORGANISM: Homo sapiens						
US-10-247-685-2						
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Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	MSQTGSPGRGLAGRWMGA.....LHRRAQFILEBILRRRPWAGRK	1	MSQTGSPGRGLAGRWMGA.....LHRRAQFILEBILRRRPWAGRK	1	60
Db	1	MSQTGSPGRGLAGRWMGA.....LHRRAQFILEBILRRRPWAGRK	1	MSQTGSPGRGLAGRWMGA.....LHRRAQFILEBILRRRPWAGRK	1	60
Qy	61	IVPFBKLNGSVLPGSAGAPRLCRQLQAFGSTLILBQDSGVQYEGTLVQLGQAFBLLG	61	IVPFBKLNGSVLPGSAGAPRLCRQLQAFGSTLILBQDSGVQYEGTLVQLGQAFBLLG	120	
Db	61	IVPFBKLNGSVLPGSAGAPRLCRQLQAFGSTLILBQDSGVQYEGTLVQLGQAFBLLG	61	IVPFBKLNGSVLPGSAGAPRLCRQLQAFGSTLILBQDSGVQYEGTLVQLGQAFBLLG	120	
Qy	121	GAEGTYLTGTGTDPESTASLHDGQALGVQYRGAELHQLPQEGTTPNSAGGPQEGTTPNSAGGPQEGT	121	GAEGTYLTGTGTDPESTASLHDGQALGVQYRGAELHQLPQEGTTPNSAGGPQEGT	180	
Db	121	GAEGTYLTGTGTDPESTASLHDGQALGVQYRGAELHQLPQEGTTPNSAGGPQEGT	121	GAEGTYLTGTGTDPESTASLHDGQALGVQYRGAELHQLPQEGTTPNSAGGPQEGT	180	
Qy	181	LRKSPASSQGPMPNVAQDGSPPRPEAKRASLRSREVETLVAADDNAFHGGGLKR	181	LRKSPASSQGPMPNVAQDGSPPRPEAKRASLRSREVETLVAADDNAFHGGGLKR	240	

Db	181	LRRKSPASQQGPMCNVKAPLGSPSPRRAKRFASLSRFETLVADDKMAAFHGAGLKR	240	1	MSQTGSHPGRLAGRWGQCPCLLPIVPLSWLWLLILASPLPREEE	60
Qy	241	YLITVMAAAAKAFKHPSPRNPLVSLVTRLVLIGSGEIGPQVQPSAAOTLRSACWORGLN	300	61	IVFPEKLNGSYLPGSCAPARLCLQAFGETLLELQDSGVQVEGLTIVQLGQAPELLG	120
Db	241	YLITVMAAAAKAFKHPSPRNPLVSLVTRLVLIGSGEIGPQVQPSAAOTLRSACWORGLN	300	61	IVFPEKLNGSYLPGSCAPARLCLQAFGETLLELQDSGVQVEGLTIVQLGQAPELLG	120
Qy	301	TPEDSDPDPHDTAILFTQDLGCVSTCDLGMADGYTCDPARSCALVEDDGLQSAFTAA	360	121	GAEPGTYLTGTINGDPEVASLHWGDGALICVQYRGAELHLOPLEGGTNSAGGGAAHI	180
Db	301	TPEDSDPDPHDTAILFTQDLGCVSTCDLGMADGYTCDPARSCALVEDDGLQSAFTAA	360	121	GAEPGTYLTGTINGDPEVASLHWGDGALICVQYRGAELHLOPLEGGTNSAGGGAAHI	180
Qy	361	HELGHVNMLHDNSKPCISLNGPLSTSRRHMAAPMAYDPEPWSPCSARFTIDFLDNGY	420	181	LRRKSPASQQGPMCNVKAPLGSPSPRRAKRFASLSRFETLVADDKMAAFHGAGLKR	240
Db	361	HELGHVNMLHDNSKPCISLNGPLSTSRRHMAAPMAYDPEPWSPCSARFTIDFLDNGY	420	181	LRRKSPASQQGPMCNVKAPLGSPSPRRAKRFASLSRFETLVADDKMAAFHGAGLKR	240
Qy	421	GHCLDKDPKAAPLHLPPVTPGKDYDADROQLTQGDSSCPOLPPCAALWCSGHNLGA	480	241	YLITVMAAAAKFKHSPRNPLVSLVTRLVLIGSGEIGPQVQPSAAOTLRSACWORGLN	300
Db	421	GHCLDKDPKAAPLHLPPVTPGKDYDADROQLTQGDSSCPOLPPCAALWCSGHNLGA	480	241	YLITVMAAAAKFKHSPRNPLVSLVTRLVLIGSGEIGPQVQPSAAOTLRSACWORGLN	300
Qy	481	MCQTKHSPWADGTPCPGAQACMGCRCLHMDOLODFTNFIQAGERGPMGPWGDCSRTEGGV	540	301	TPEDSDPDPHDTAILFTQDLGCVSTCDLGMADYTVCDPARSCALVEDDGLQSAFTAA	360
Db	481	MCQTKHSPWADGTPCPGAQACMGCRCLHMDOLODFTNFIQAGERGPMGPWGDCSRTEGGV	540	301	TPEDSDPDPHDTAILFTQDLGCVSTCDLGMADYTVCDPARSCALVEDDGLQSAFTAA	360
Qy	541	QFSSRDCTRPVPNRGCKYCEGRTRPNSCTEDCPTGSALTFREBQAAYNHRTDLFKSF	600	361	HELGHVNMLHDNSKPCISLNGPLSTSRRHMAAPMAYDPEPWSPCSARFTIDFLDNGY	420
Db	541	QFSSRDCTRPVPNRGCKYCEGRTRPNSCTEDCPTGSALTFREBQAAYNHRTDLFKSF	600	361	HELGHVNMLHDNSKPCISLNGPLSTSRRHMAAPMAYDPEPWSPCSARFTIDFLDNGY	420
Qy	601	PGPMDWVPRYTTGAPDQCKLTCOARALGYYTLEPRVWDGFCPCSPLOSSVVCYQGRTHA	660	421	GHCLDKPPEAHLPPVTPGKDYDADROQCOLTEGPSPSRHCPOLPPCAALWCSGHNLGA	480
Db	601	PGPMDWVPRYTTGAPDQCKLTCOARALGYYTLEPRVWDGFCPCSPLOSSVVCYQGRTHA	660	421	GHCLDKPPEAHLPPVTPGKDYDADROQCOLTEGPSPSRHCPOLPPCAALWCSGHNLGA	480
Qy	661	GCDRIGSCKKFDICMVGCGDGSCKSKQGSFSPKFRYGNVNTYTIpagathLILVQGQNP	720	481	MCQTKHSPWADGTPCPGAQACMGCRCLHMDOLODFTNIPQAGCWMGPWGDCSRTEGGV	540
Db	661	GCDRIGSCKKFDICMVGCGDGSCKSKQGSFSPKFRYGNVNTYTIpagathLILVQGQNP	720	481	MCQTKHSPWADGTPCPGAQACMGCRCLHMDOLODFTNIPQAGCWMGPWGDCSRTEGGV	540
Qy	721	GHRSTYLAALKLPDGSYALNGEYTLIMSPSPDVLPGAVSLRYSGATASETLSSGHGPLAQ	780	541	QFSSRDCTRPVPNRGCKYCEGRTRPNSCTEDCPTGSALTFREBQAAYNHRTDLFKSF	600
Db	721	GHRSTYLAALKLPDGSYALNGEYTLIMSPSPDVLPGAVSLRYSGATASETLSSGHGPLAQ	780	541	QFSSRDCTRPVPNRGCKYCEGRTRPNSCTEDCPTGSALTFREBQAAYNHRTDLFKSF	600
Qy	781	LTLQVLVAGNPQDTLRLYSSEFPVRPTPSTPRPQDMLHRRQAQILELIRRTPWAGRK	837	601	PGMDWVPRYTTGAPDQCKLTCQARALGYYTLEPRVWDGFCPCSPLOSSVVCYQGRTHA	660
Db	781	LTLQVLVAGNPQDTLRLYSSEFPVRPTPSTPRPQDMLHRRQAQILELIRRTPWAGRK	837	601	PGMDWVPRYTTGAPDQCKLTCQARALGYYTLEPRVWDGFCPCSPLOSSVVCYQGRTHA	660
Qy	837	RESULT 2		661	GCDRIGSCKKFDICMVGCGDGSCKSKQGSFSPKFRYGNVNTYTIpagathLILVQGQNP	720
Db	837	US-10-408-765A-1349		661	GCDRIGSCKKFDICMVGCGDGSCKSKQGSFSPKFRYGNVNTYTIpagathLILVQGQNP	720
Qy	837	sequence 1-348, Application US/10408765A		721	GRHSIYLAALKLPDGSYALNGEYTLIMSPSPDVLPGAVSLRYSGATASETLSSGHGPLAQ	780
Db	837	Publication No. US20040101874A1		721	GRHSIYLAALKLPDGSYALNGEYTLIMSPSPDVLPGAVSLRYSGATASETLSSGHGPLAQ	780
Qy	837	GENERAL INFORMATION:				
Db	837	APPLICANT: Ghosh, Soumitra S.				
Qy	837	APPLICANT: Fahy, Eoin D.				
Db	837	APPLICANT: Zhang, Bing				
Qy	837	APPLICANT: Gibson, Bradford W.				
Db	837	APPLICANT: Taylor, Steven W.				
Qy	837	APPLICANT: Glenn, Gary M.				
Db	837	APPLICANT: Warnock, Dale E.				
Qy	837	TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION				
Db	837	TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME				
Qy	837	FILE REFERENCE: 66008-465				
Db	837	SEQUENCE 1, Application US/10628432				
Qy	837	CURRENT APPLICATION NUMBER: US/10/408765A				
Db	837	CURRENT FILING DATE: 2003-04-04				
Qy	837	NUMBER OF SEQ ID NOS: 3077				
Db	837	SOFTWARE: FastSEQ for Windows Version 4.0				
Qy	837	SEQ ID NO: 1348				
Db	837	LENGTH: 837				
Qy	837	TYPE: PRT				
Db	837	ORGANISM: Homo sapiens				
Qy	837	US-10-408-765A-1348				
Db	837	Query Match 100.0%; Score 4570; DB 16; Length 837;				
Qy	837	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;				
Db	837	Matches 837; Conservation 0;				
Qy	837	1 MSQTGSHPGRLAGRWGQCPCLLPIVPLSWLWLLILASPLPREEE 60				

Query Match 100.0%; Score 4570; DB 16; Length 837;
 Best Local Similarity 100.0%; Prod. No. 0;
 Matches 837; Conservative 0; Mismatches 0; Gaps 0;
 Db 1 MSQTGSHPGRGLACRWLWQAQPCUCLLPIVPLSWLWLLLLASPLPREE 60
 Db 1 MSQTGSHPGRGLACRWLWQAQPCUCLLPIVPLSWLWLLLLASPLPREE 60

Qy 61 IVPEBKLNQSVLPSGAPARLICRQAFETLLEQDGSVYCEGITYQYLGQAPELG 120
 Db 61 IVPEBKLNQSVLPSGAPARLICRQAFETLLEQDGSVYCEGITYQYLGQAPELG 120

Qy 121 GABPGTYLTGTINGDPESTASLHNDGGALGIVQYRGAEHLQPLEGTPNSGGPGAH 180
 Db 121 GABPGTYLTGTINGDPESTASLHNDGGALGIVQYRGAEHLQPLEGTPNSGGPGAH 180

Qy 181 LRRKSPASSQGPMCNVKALGSPPRPRAKRFASSLRVEVTLVADDKMAAFHGAGIKR 240
 Db 181 LRRKSPASSQGPMCNVKALGSPPRPRAKRFASSLRVEVTLVADDKMAAFHGAGIKR 240

Qy 241 YLTIVMAAAKAKAFAKHPSPTRNPVSLVYTRIVLGSGEREFGVQGSAATLRSFCAWQRGLN 300
 Db 241 YLTIVMAAAKAKAFAKHPSPTRNPVSLVYTRIVLGSGEREFGVQGSAATLRSFCAWQRGLN 300

Qy 301 TPEDSDPDPHDFTAILFTQDLGCVSTCDTGADVGTVCDPARSCATVDDGQOSATTA 360
 Db 301 TPEDSDPDPHDFTAILFTQDLGCVSTCDTGADVGTVCDPARSCATVDDGQOSATTA 360

Qy 361 HEGLHVNFMNLHDNSKPCISLNGPLJSTSRHMAPVMAHYDPEEWSPCSARFTIDFLONGY 420
 Db 361 HEGLHVNFMNLHDNSKPCISLNGPLJSTSRHMAPVMAHYDPEEWSPCSARFTIDFLONGY 420

Qy 421 GHCLDKPAPLILPVTPGKDYDADROQLTGPDSHCPOLPPCAALWCSGHUNGHA 480
 Db 421 GHCLDKPAPLILPVTPGKDYDADROQLTGPDSHCPOLPPCAALWCSGHUNGHA 480

Qy 481 MCQTKHSPWADGTPCGPAQACMGCRCLHMDQLODENTIQAAGGNGPQWGDCSRTCGGV 540
 Db 481 MCQTKHSPWADGTPCGPAQACMGCRCLHMDQDFNTIQAAGGNGPQWGDCSRTCGGV 540

Qy 541 QFSSRDCTRPVPRANGKTYCEGRTRFRSNTEDCPTGSAALTERBQAZAYNERTDLPKS F 600
 Db 541 QFSSRDCTRPVPRANGKTYCEGRTRFRSNTEDCPTGSAALTERBQAZAYNERTDLPKS F 600

Qy 601 PGMDWVPRYRTGTAPODQCKLTQCARALGYYTLEPRVDTGPSCPDSSSVCYQGRCHTA 660
 Db 601 PGMDWVPRYRTGTAPODQCKLTQCARALGYYTLEPRVDTGPSCPDSSSVCYQGRCHTA 660

Qy 661 GCDRIIGSKKKPDKCMVCGDGGCSKOSGFSRKFRKRYCYYNTIPIAGATHILVRQGNP 720
 Db 661 GCDRIIGSKKKPDKCMVCGDGGCSKOSGFSRKFRKRYCYYNTIPIAGATHILVRQGNP 720

Qy 721 GRSIYLAALKLPDGSYALNGEYTMLPSPDTVLPGAVSLRYSGATASETLSGHGPLAQ P 780
 Db 721 GRSIYLAALKLPDGSYALNGEYTMLPSPDTVLPGAVSLRYSGATASETLSGHGPLAQ P 780

Qy 781 LTLQVLVAGNPQDTRLRYSFFVRPTPSPDTVLPGAVSLRYSGATASETLSGHGPLAQ 837
 Db 781 LTLQVLVAGNPQDTRLRYSFFVRPTPSPDTVLPGAVSLRYSGATASETLSGHGPLAQ 837

RESULT 4
 US-10-628-132-29
 Sequence 29, Application US/10628432
 Publication No. US20140142863A1
 GENERAL INFORMATION:
 APPLICANT: Wyeth
 TITLE OF INVENTION: Modified ADAMTS4 molecules
 FILE REFERENCE: AN101378
 CURRENT APPLICATION NUMBER: US/10/628, 432
 CURRENT FILING DATE: 2003-07-29
 NUMBER OF SEQ ID NOS: 53

RESULT 5
 US-10-358-283-11
 Sequence 11, Application US/10358283

Qy	781	LTLQVLAGNPODTRLRKFVVRPPTSPRPPQDWLHRRAQILELRRPAGRK 837
Db	781	LTLQVLAGNPODTRLRKFVVRPPTSPRPPQDWLHRRAQILELRRPAGRK 837
		RESULT 6
	US-19-946-374-317	Sequence 317, Application US/09946374
		Publication No. US20030073129A1
		GENERAL INFORMATION:
	/	APPLICANT: Baker, Kevin P.
	/	APPLICANT: Borsstein, David
	/	APPLICANT: Destroyers, Luc
	/	APPLICANT: Eaton, Dan L.
	/	APPLICANT: Ferrara, Napoleone
	/	APPLICANT: Fong, Sherman
	/	APPLICANT: Gao, Wei-Qiang
	/	APPLICANT: Goddard, Audrey
	/	APPLICANT: Godowski, Paul J.
	/	APPLICANT: Grimaldi, Christopher J.
	/	APPLICANT: Gurney, Austin L.
	/	APPLICANT: Hillan, Kenneth J.
	/	APPLICANT: Pan, James
	/	APPLICANT: Paoni, Nicholas F.
	/	APPLICANT: Roy, Margaret Ann
	/	APPLICANT: Smith, Victoria
	/	APPLICANT: Stewart, Timothy A.
	/	APPLICANT: Tunas, Daniel
	/	APPLICANT: Watanabe, Colin K.
	/	APPLICANT: Williams, P. Mickey
	/	APPLICANT: Wood, William I.
		TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
		TITLE OF INVENTION: Acids Encoding the Same
		FILE REFERENCE: P2830B1C1
		CURRENT APPLICATION NUMBER: US/09/946,374
		CURRENT FILING DATE: 2001-09-04
	/	PRIOR APPLICATION NUMBER: 60/0987116
	/	PRIOR FILING DATE: 1998-09-01
	/	PRIOR APPLICATION NUMBER: 60/098723
	/	PRIOR FILING DATE: 1998-09-01
	/	PRIOR APPLICATION NUMBER: 60/098749
	/	PRIOR FILING DATE: 1998-09-01
	/	PRIOR APPLICATION NUMBER: 60/098750
	/	PRIOR FILING DATE: 1998-09-01
	/	PRIOR APPLICATION NUMBER: 60/098803
	/	PRIOR FILING DATE: 1998-09-02
	/	PRIOR APPLICATION NUMBER: 60/098821
	/	PRIOR FILING DATE: 1998-09-02
	/	PRIOR APPLICATION NUMBER: 60/098843
	/	PRIOR FILING DATE: 1998-09-02
	/	PRIOR APPLICATION NUMBER: 60/099536
	/	PRIOR FILING DATE: 1998-09-09
	/	PRIOR APPLICATION NUMBER: 60/099596
	/	PRIOR FILING DATE: 1998-09-09
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	/	PRIOR FILING DATE: 1998-09-09
	/	PRIOR APPLICATION NUMBER: 60/099602
	/	PRIOR FILING DATE: 1998-09-09
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	/	PRIOR FILING DATE: 1998-09-09
	/	PRIOR APPLICATION NUMBER: 60/099741
	/	PRIOR FILING DATE: 1998-09-10
	/	PRIOR APPLICATION NUMBER: 60/099754
	/	PRIOR FILING DATE: 1998-09-10
	/	PRIOR APPLICATION NUMBER: 60/099763
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	/	PRIOR FILING DATE: 1998-09-10

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PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100385
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PRIOR FILING DATE: 1998-09-16
PRIOR APPLICATION NUMBER: 60/100662
PRIOR FILING DATE: 1998-05-16
PRIOR APPLICATION NUMBER: 60/100664
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PRIOR APPLICATION NUMBER: 60/100683
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PRIOR APPLICATION NUMBER: 60/100684
PRIOR FILING DATE: 1998-05-17
PRIOR APPLICATION NUMBER: 60/100710
PRIOR FILING DATE: 1998-05-17
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PRIOR FILING DATE: 1998-09-17
PRIOR APPLICATION NUMBER: 60/100848
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100849
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/100919
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/100930
PRIOR FILING DATE: 1998-05-17
PRIOR APPLICATION NUMBER: 60/101014
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PRIOR APPLICATION NUMBER: 60/101068
PRIOR FILING DATE: 1998-09-18
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PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: 60/101279
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/101475
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101476
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/101477
PRIOR FILING DATE: 1998-05-23
PRIOR APPLICATION NUMBER: 60/101479
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PRIOR APPLICATION NUMBER: 60/101738
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101741
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/101743
PRIOR FILING DATE: 1998-05-24
PRIOR APPLICATION NUMBER: 60/101915
PRIOR FILING DATE: 1998-05-24
PRIOR APPLICATION NUMBER: 60/101916
PRIOR FILING DATE: 1998-09-24
PRIOR APPLICATION NUMBER: 60/102207
PRIOR FILING DATE: 1998-05-29
PRIOR APPLICATION NUMBER: 60/102240
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 60/102307

Query Match	99.8%	Score 4563;	DB 10;	Length 837;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches	836;	Conservative	0;	
		Mismatches	1;	
		Indels	0;	
		Gaps	0;	
1	MSQTGSHPGRLAGRMWGAQPCILLEPVLPIPLSMLWVWILLILLASLPSARLASLPLPREE	60		
1	MSQTGSHPGRLAGRMWGAQPCILLEPVLPIPLSMLWVWILLILLASLPSARLASLPLPREE	60		
61	IVPEPKINGSVLPGSGAPARLICRLOFGETTLELBDGIVQEVGLTVQYLGAPELLG	120		
61	IVPEPKINGSVLPGSGAPARLICRLOFGETTLELBDGIVQEVGLTVQYLGAPELLG	120		
61	IVPEPKINGSVLPGSGAPARLICRLOFGETTLELBDGIVQEVGLTVQYLGAPELLG	120		

a D a D

Qy 121 GAAEPTYLTTGTINGDPESVASTLHWDDGALLGVLYQTRGAELHNPQPLEGGTNSAGGGAAH 180
 Qy 121 GAAEPTYLTTGTINGDPESVASTLHWDDGALLGVLYQTRGAELHNPQPLEGGTNSAGGGAAH 180
 Db 121 GAAEPTYLTTGTINGDPESVASTLHWDDGALLGVLYQTRGAELHNPQPLEGGTNSAGGGAAH 180
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
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 ; PRIOR APPLICATION NUMBER: 60/063564
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063734
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063870
 ; PRIOR FILING DATE: 1997-10-31
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 ; PRIOR APPLICATION NUMBER: 60/065311
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 ; PRIOR FILING DATE: 1997-11-21
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 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/081049
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 ; PRIOR APPLICATION NUMBER: 60/081070
 ; PRIOR FILING DATE: 1998-04-08
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 ; PRIOR APPLICATION NUMBER: 60/081838
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082568
 ; PRIOR FILING DATE: 1998-04-21
 ; PRIOR APPLICATION NUMBER: 60/082569
 ; PRIOR FILING DATE: 1997-09-18

RESULT 7
 US-10-052-586-352
 Publication No. US20020127594A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ACIDS ENCODING THE SAME
 FILE REFERENCE: P3430R1CL
 CURRENT APPLICATION NUMBER: US10/052,586
 CURRENT FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082704
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/083322
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 PRIOR APPLICATION NUMBER: 60/083495
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 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084414
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 PRIOR APPLICATION NUMBER: 60/084640
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 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
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 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088722
 PRIOR FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
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 PRIOR APPLICATION NUMBER: 60/089166
 PRIOR FILING DATE: 1998-06-12
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 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089908
 Query Match 99.8%; Score 4563; DB 13; Length 837;
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 836; Conservative 0; Indels 0; Gaps 0;
 Qy 1 MSQTGSHPGRGLAGRNWQAGPCLLPIVPLSWLWNLILLASLPSARLASPLPREEB 60
 Db 1 MSQTGSHPGRGLAGRNWQAGPCLLPIVPLSWLWNLILLASLPSARLASPLPREEB 60
 Qy 61 IVFPEKLNGSLVPGSGAPARLICRQAFGETLLEQDSGVQEGLTVQYQGQAPELGL 120
 Db 61 IVFPEKLNGSLVPGSGAPARLICRQAFGETLLEQDSGVQEGLTVQYQGQAPELGL 120
 Qy 121 GAEPGTYLTGTGTINGDPESVASHWDGAGLGYQYRGAEHLQPLEEGTPNSAGGPAGHL 180
 Db 121 GAEPGTYLTGTGTINGDPESVASHWDGAGLGYQYRGAEHLQPLEEGTPNSAGGPAGHL 180
 Qy 181 LRRKSPASQGQGMNCYVAPLGSPPSPRRAKRFASLSRFVETLVADDKMAAFHAGLKR 240
 Db 181 LRRKSPASQGQGMNCYVAPLGSPPSPRRAKRFASLSRFVETLVADDKMAAFHAGLKR 240
 Qy 241 YLTVMAAAAKAFKHPSPTRNPVSLVYTRVLGSGEEGPQYQGSPSAOTLRSFCAWQGLN 300
 Db 241 YLTVMAAAAKAFKHPSPTRNPVSLVYTRVLGSGEEGPQYQGSPSAOTLRSFCAWQGLN 300
 Qy 301 TPBDSDPHDFTAILTRQDLCGVSTCDLGMADYGTCDPARSCLATEDDGHQSAPTA 360
 Db 301 TPBDSDPHDFTAILTRQDLCGVSTCDLGMADYGTCDPARSCLATEDDGHQSAPTA 360
 Qy 361 HELGHYFNMLHDNSKPCISLNGPLSRHVMAPVMAHDPPEPWSPCSARFTTDPLONGY 420
 Db 361 HELGHYFNMLHDNSKPCISLNGPLSRHVMAPVMAHDPPEPWSPCSARFTTDPLONGY 420
 Qy 421 GHCLLDKPEAHLPLTPGKDYDAHQCOLTFTGPDSPSRHCPOLPPCAALNCGSHLNHG 480
 Db 421 GHCLLDKPEAHLPLTPGKDYDAHQCOLTFTGPDSPSRHCPOLPPCAALNCGSHLNHG 480
 Qy 481 MCOTKSPWADGTPCGPAQACMGRCUHMDQLQDENIPQAGGMGPNGPWGDCSRTCGGGV 540
 Db 481 MCOTKSPWADGTPCGPAQACMGRCUHMDQLQDENIPQAGGMGPNGPWGDCSRTCGGGV 540

Qy	541 QFSSRDCTRPVPRNGGKYCEGRRTRPRSCNTEDCPTGSALTFREEQCAAANHRTDLFKSF 600 QFSSRDCTRPVPRNGGKYCEGRRTRPRSCNTEDCPTGSALTFREEQCAAANHRTDLFKSF 600	Db	241 YLTVMAAAAKAPKPHPSIRNPVSLVTRVLIGSGBEPQVGPSAAQTLSFCAWQCLN 300 301 TPEBOSDPRFDTALLPTDLCGYSTCDTLMADVGTCPRASCAIYEDDGLOSATAA 360 301 TPEDSGPDPHDFTDALLPTDLCGYSTCDTLMADVGTCPRASCAIYEDDGLOSATAA 360
Db	601 PGMDWTPRGTGYAPQDCKLTCQARALGYYTLEPRVVDCTPCSPDSSSYCQGRCIHA 660 PGMDWTPRGTGYAPQDCKLTCQARALGYYTLEPRVVDCTPCSPDSSSYCQGRCIHA 660	Db	361 HELGFIVNMILHDNSKPCITSLNGPLJSTSHVMAPVMAHYDPEPMSPSCARPTIDELDNGY 420 361 HELGFIVNMILHDNSKPCITSLNGPLJSTSHVMAPVMAHYDPEPMSPSCARPTIDELDNGY 420
Qy	661 GCDRIGSKRKFDKCMYCGDSSGCKTOSGSPRKFRGYGNNVTIPAGATHILVRQGNP 720 GCDRIGSKRKFDKCMYCGDSSGCKTOSGSPRKFRGYGNNVTIPAGATHILVRQGNP 720	Db	361 HELGFIVNMILHDNSKPCITSLNGPLJSTSHVMAPVMAHYDPEPMSPSCARPTIDELDNGY 420 361 HELGFIVNMILHDNSKPCITSLNGPLJSTSHVMAPVMAHYDPEPMSPSCARPTIDELDNGY 420
Qy	721 GHSIYLAALKPDPSYALNGETTMLMPSPTDVVLPGAVSLRYSGATASETSLGHGPLAQ 780 721 GHSIYLAALKPDPSYALNGETTMLMPSPTDVVLPGAVSLRYSGATASETSLGHGPLAQ 780	Db	481 MCQTKHSPMDGTPCGPAQACMGGRCLHMDQDQDENIPOAGGNGPWPWGDCSRTEGGYV 540 481 MCQTKHSPMDGTPCGPAQACMGGRCLHMDQDQDENIPOAGGNGPWPWGDCSRTEGGYV 540
Db	781 LTLOQVLAQNPQDTRLRYSPFVPRPTPSPTRPTPQDWLHRRAQILELIRRPWAGRK 837 781 LTLOQVLAQNPQDTRLRYSPFVPRPTPSPTRPTPQDWLHRRAQILELIRRPWAGRK 837	Db	541 QFSSRDCTRPVPRNGGKYCEGRRTRPRSCNTEDCPTGSALTFREEQCAAYNHRDLFKSF 600 541 QFSSRDCTRPVPRNGGKYCEGRRTRPRSCNTEDCPTGSALTFREEQCAAYNHRDLFKSF 600
Db	781 LTLOQVLAQNPQDTRLRYSPFVPRPTPSPTRPTPQDWLHRRAQILELIRRPWAGRK 837 781 LTLOQVLAQNPQDTRLRYSPFVPRPTPSPTRPTPQDWLHRRAQILELIRRPWAGRK 837	Db	601 PGPMMDWVPRITGVAPDQCKLTCAARALGYYLEPRVVDGTPCSPDSSSVCYQGRCIHA 660 601 PGPMMDWVPRITGVAPDQCKLTCAARALGYYLEPRVVDGTPCSPDSSSVCYQGRCIHA 660
RESULT 8			
US-10-174-590-352			
; Sequence 32, Application US/10174590			
; Publication No. US20030008352A1.			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Chen, Jian			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Godard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Pan, James			
; APPLICANT: Smith, Victoria			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; ACIDS ENCODING THE SAME			
; FILE REFERENCE: P3430R1C42			
; CURRENT APPLICATION NUMBER: US/10/174,590			
; CURRENT FILING DATE: 2002-06-18			
; Prior application removed - See File Wrapper or Palm			
; NUMBER OF SEQ ID NOS: 612			
; SEQ ID NO: 352			
; LENGTH: 837			
; TYPE: PRT			
; ORGANISM: Homo Sapien			
US-10-174-590-352			
Query Match 99.8%; Score 4563; DB 14; Length 837;			
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Gaps 0;			
Matches 836; Conservative 0; Mismatches 0; Gaps 0;			
Qy			
1 MSQTGSHPGRGLAGRMWGAQCLLPIVPLSWLWILLILLASLPSRLASPLPREE 60			
1 MSQTGSHPGRGLAGRMWGAQCLLPIVPLSWLWILLILLASLPSRLASPLPREE 60			
61 IVFPEKINGSVLPGSGAPARLICRQAFGETLLEQDSEVOEGTLVYQLQAPELLG 120			
61 IVFPEKINGSVLPGSGAPARLICRQAFGETLLEQDSEVOEGTLVYQLQAPELLG 120			
61 GAEPGTYLTGTGTDPESSVSHWDGCAALLGVLQPLGGTNSAGPGAAH 180			
61 GAEPGTYLTGTGTDPESSVSHWDGCAALLGVLQPLGGTNSAGPGAAH 180			
181 LARKSPASQGGMNTVAKPLGSPSPRRAKRFAASLQVPLSLVTRVLIGSGBEGQVQGPSAAQTLSFCAWQCLN 300			
181 LARKSPASQGGMNTVAKPLGSPSPRRAKRFAASLQVPLSLVTRVLIGSGBEGQVQGPSAAQTLSFCAWQCLN 300			
Qy			
241 YLTVMAAAAKAPKPHPSIRNPVSLVTRVLIGSGBEPQVGPSAAQTLSFCAWQCLN 300			
241 YLTVMAAAAKAPKPHPSIRNPVSLVTRVLIGSGBEPQVGPSAAQTLSFCAWQCLN 300			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; ACIDS ENCODING THE SAME			
; FILE REFERENCE: P3430R1C42			
; CURRENT APPLICATION NUMBER: US/10/176,758			
; CURRENT FILING DATE: 2002-06-21			
; Prior application removed - See File Wrapper or Palm			
; NUMBER OF SEQ ID NOS: 612			
; SEQ ID NO: 352			
; LENGTH: 837			
; TYPE: PRT			
; ORGANISM: Homo Sapien			
US-10-176-758-352			
Query Match 99.8%; Score 4563; DB 14; Length 837;			
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Gaps 0;			
Matches 836; Conservative 0; Mismatches 1; Gaps 0;			
Qy			
1 MSQTGSHPGRGLAGRMWGAQCLLPIVPLSWLWILLILLASLPSRLASPLPREE 60			

|||||||
1 MSQTGSHPGRGLAQRWLGQPCLLPIVPJSWLLLTLASLPSARLASPLPREE 60
Db 61 IVPEKINGSVLPGSGAPARLICRLQAFGETLLEIQRDGSVQVEGLTIVQYIQLQAPELLG 120
Qy 61 IVPEKINGSVLPGSGAPARLICRLQAFGETLLEIQRDGSVQVEGLTIVQYIQLQAPELLG 120
Db 61 IVPEKINGSVLPGSGAPARLICRLQAFGETLLEIQRDGSVQVEGLTIVQYIQLQAPELLG 120
Qy 121 GAEPTGYLTGTINGDPSSVASHWDGALLGIVLQPLGGTNPSSAGGGAAH 180
Db 121 GAEPTGYLTGTINGDPSSVASHWDGALLGIVLQPLGGTNPSSAGGGAAH 180
Qy 181 LRKSPASGGQPMCNVKAFLGSPSPRRAKRFAISLRFVETLWADDKMAFHRGAGLKR 240
Db 181 LRKSPASGGQPMCNVKAFLGSPSPRRAKRFAISLRFVETLWADDKMAFHRGAGLKR 240
Qy 241 YLTIVMAAAFLAKFKHPSRNPVSLVTRVLIQGSGBEGPQVQPSAQTLLRFCAWORGLN 300
Db 241 YLTIVMAAAFLAKFKHPSRNPVSLVTRVLIQGSGBEGPQVQPSAQTLLRFCAWORGLN 300
Qy 301 TREDSPDPHFDPAILPFTQDLGVSTCDLGMADGTVCDPARSACIVEDGQLSAFTAA 360
Db 301 TPDSDGPDHFDPAILPFTQDLGVSTCDLGMADGTVCDPARSACIVEDGQLSAFTAA 360
Qy 361 HBLGHVFMHDNSKPCISLNGPLS1STRHNPSSARFPTTDFLDNGY 420
Db 361 HBLGHVFMHDNSKPCISLNGPLS1STRHNPSSARFPTTDFLDNGY 420
Qy 421 GHLLDKPKEAPLHLPVTFPGKDYDADPQCLTTFGPDSRHCPCOLPPCAALWCSGHNLNGHA 480
Db 421 GHLLDKPKEAPLHLPVTFPGKDYDADPQCLTTFGPDSRHCPCOLPPCAALWCSGHNLNGHA 480
Qy 481 MCQTKASPSWADGTPCPGAQACMGRCLHMDQDENIPOAGCWGPMGPWDGCSRTCGGY 540
Db 481 MCQTKASPSWADGTPCPGAQACMGRCLHMDQDENIPOAGCWGPMGPWDGCSRTCGGY 540
Qy 541 QFSSRDCTRPVERNGKYCEGRTRFRSNCNTEDCPTPSALTRFREQAAATHRTDLFKSF 600
Db 541 QFSSRDCTRPVERNGKYCEGRTRFRSNCNTEDCPTPSALTRFREQAAATHRTDLFKSF 600
Qy 601 PGPMWDWYPRYTYGAPODQCKLTQCARALGTYYLEPRVVDGTPCSDPSSSYCVOGRCIHA 660
Db 601 PGPMWDWYPRYTYGAPODQCKLTQCARALGTYYLEPRVVDGTPCSDPSSSYCVOGRCIHA 660
Qy 661 GCDRIGSKKEDKCMVCGDGSCKQSFRKFRYGYNNVTIAGATHILVRQGNP 720
Db 661 GCDRIGSKKEDKCMVCGDGSCKQSFRKFRYGYNNVTIAGATHILVRQGNP 720
Qy 721 GHRSTYIALKLPDGSYALNGBTMPLMPSTPDTVLPGAVSLRYSGATASETLSGHGLAQP 780
Db 721 GHRSTYIALKLPDGSYALNGBTMPLMPSTPDTVLPGAVSLRYSGATASETLSGHGLAQP 780
Qy 781 LTLQVIVAGNPQDTRIYSPFVPRPTPSTPRETPDQLHRAQILELRRPWAERK 837
Db 781 LTLQVIVAGNPQDTRIYSPFVPRPTPSTPRETPDQLHRAQILELRRPWAERK 837

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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: B34301C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO: 352
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-175-137-352

Query Match 99.8%; Score 4563; DB 14; Length 837;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 836; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;

Qy 1 MSQTGSHPGRGLAQRWLGQPCLLPIVPJSWLLLTLASLPSARLASPLPREE 60
Db 1 MSQTGSHPGRGLAQRWLGQPCLLPIVPJSWLLLTLASLPSARLASPLPREE 60
Qy 61 IVPEKINGSVLPGSGAPARLICRLQAFGETLLEIQRDGSVQVEGLTIVQYIQLQAPELLG 120
Db 61 IVPEKINGSVLPGSGAPARLICRLQAFGETLLEIQRDGSVQVEGLTIVQYIQLQAPELLG 120
Qy 121 GAEPTGYLTGTINGDPSSVASHWDGALLGIVLQPLGGTNPSSAGGGAAH 180
Db 121 GAEPTGYLTGTINGDPSSVASHWDGALLGIVLQPLGGTNPSSAGGGAAH 180
Qy 181 LRKSPASGGQPMCNVKAFLGSPSPRRAKRFAISLRFVETLWADDKMAFHRGAGLKR 240
Db 181 LRKSPASGGQPMCNVKAFLGSPSPRRAKRFAISLRFVETLWADDKMAFHRGAGLKR 240
Qy 241 YLTIVMAAAFLAKFKHPSRNPVSLVTRVLIQGSGBEGPQVQPSAQTLLRFCAWORGLN 300
Db 241 YLTIVMAAAFLAKFKHPSRNPVSLVTRVLIQGSGBEGPQVQPSAQTLLRFCAWORGLN 300
Qy 301 TREDSPDPHFDPAILPFTQDLGVSTCDLGMADGTVCDPARSACIVEDGQLSAFTAA 360
Db 301 TPDSDGPDHFDPAILPFTQDLGVSTCDLGMADGTVCDPARSACIVEDGQLSAFTAA 360
Qy 361 HBLGHVFMHDNSKPCISLNGPLS1STRHNPSSARFPTTDFLDNGY 420
Db 361 HBLGHVFMHDNSKPCISLNGPLS1STRHNPSSARFPTTDFLDNGY 420
Qy 421 GHLLDKPKEAPLHLPVTFPGKDYDADPQCLTTFGPDSRHCPCOLPPCAALWCSGHNLNGHA 480
Db 421 GHLLDKPKEAPLHLPVTFPGKDYDADPQCLTTFGPDSRHCPCOLPPCAALWCSGHNLNGHA 480
Qy 481 MCQTKASPSWADGTPCPGAQACMGRCLHMDQDENIPOAGCWGPMGPWDGCSRTCGGY 540
Db 481 MCQTKASPSWADGTPCPGAQACMGRCLHMDQDENIPOAGCWGPMGPWDGCSRTCGGY 540
Qy 541 QFSSRDCTRPVERNGKYCEGRTRFRSNCNTEDCPTPSALTRFREQAAATHRTDLFKSF 600
Db 541 QFSSRDCTRPVERNGKYCEGRTRFRSNCNTEDCPTPSALTRFREQAAATHRTDLFKSF 600
Qy 601 PGPMWDWYPRYTYGAPODQCKLTQCARALGTYYLEPRVVDGTPCSDPSSSYCVOGRCIHA 660
Db 601 PGPMWDWYPRYTYGAPODQCKLTQCARALGTYYLEPRVVDGTPCSDPSSSYCVOGRCIHA 660
Qy 661 GCDRIGSKKEDKCMVCGDGSCKQSFRKFRYGYNNVTIAGATHILVRQGNP 720
Db 661 GCDRIGSKKEDKCMVCGDGSCKQSFRKFRYGYNNVTIAGATHILVRQGNP 720
Qy 721 GHRSTYIALKLPDGSYALNGBTMPLMPSTPDTVLPGAVSLRYSGATASETLSGHGLAQP 780
Db 721 GHRSTYIALKLPDGSYALNGBTMPLMPSTPDTVLPGAVSLRYSGATASETLSGHGLAQP 780
Qy 781 LTLQVIVAGNPQDTRIYSPFVPRPTPSTPRETPDQLHRAQILELRRPWAERK 837
Db 781 LTLQVIVAGNPQDTRIYSPFVPRPTPSTPRETPDQLHRAQILELRRPWAERK 837

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; Sequence 352, Application US/10/175737
; Publication No. US2003001315A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanahe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

RESULT 10
US-10-175-137-352
; Sequence 352, Application US/10/175737
; Publication No. US2003001315A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanahe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

RESULT 11
 US-10-174-581-352
 / Sequence 352, Application US/10174581
 / Publication No. US2003001754041
 / GENERAL INFORMATION:
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Chen, Jian
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Pan, James
 / APPLICANT: Smith, Victoria
 / APPLICANT: Watanabe, Colin K.
 / APPLICANT: Wood, William I.
 / APPLICANT: Zhang, Zemin
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 / ACIDS ENCODING THE SAME
 / FILE REFERENCE: P3430RIC41
 / CURRENT APPLICATION NUMBER: US/10/174,581
 / CURRENT FILING DATE: 2002-06-18
 / PRIOR APPLICATION NUMBER: 10/052586
 / PRIOR FILING DATE: 2002-01-15
 / PRIOR APPLICATION NUMBER: 60/059263
 / PRIOR FILING DATE: 1997-09-18
 / PRIOR APPLICATION NUMBER: 60/059266
 / PRIOR FILING DATE: 1997-09-18
 / PRIOR APPLICATION NUMBER: 60/062250
 / PRIOR FILING DATE: 1997-10-17
 / PRIOR APPLICATION NUMBER: 60/063120
 / PRIOR FILING DATE: 1997-10-24
 / PRIOR APPLICATION NUMBER: 60/063121
 / PRIOR FILING DATE: 1997-10-24
 / PRIOR APPLICATION NUMBER: 60/063486
 / PRIOR FILING DATE: 1997-10-21
 / PRIOR APPLICATION NUMBER: 60/063540
 / PRIOR FILING DATE: 1997-10-28
 / PRIOR APPLICATION NUMBER: 60/063541
 / PRIOR FILING DATE: 1997-10-28
 / PRIOR APPLICATION NUMBER: 60/063544
 / PRIOR FILING DATE: 1997-10-28
 / PRIOR APPLICATION NUMBER: 60/063564
 / PRIOR FILING DATE: 1997-10-28
 / PRIOR APPLICATION NUMBER: 60/063734
 / PRIOR FILING DATE: 1997-10-29
 / PRIOR APPLICATION NUMBER: 60/063870
 / PRIOR FILING DATE: 1997-10-31
 / PRIOR APPLICATION NUMBER: 60/064103
 / PRIOR FILING DATE: 1997-10-31
 / PRIOR APPLICATION NUMBER: 60/065311
 / PRIOR FILING DATE: 1997-11-13
 / PRIOR APPLICATION NUMBER: 60/066120
 / PRIOR FILING DATE: 1997-11-21
 / PRIOR APPLICATION NUMBER: 60/066466
 / PRIOR FILING DATE: 1997-11-24
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 / PRIOR FILING DATE: 1997-11-24
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 / PRIOR APPLICATION NUMBER: 60/069870
 / PRIOR FILING DATE: 1997-12-17
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 / PRIOR FILING DATE: 1998-03-11
 / PRIOR APPLICATION NUMBER: 60/078886
 / PRIOR FILING DATE: 1998-03-20
 / PRIOR APPLICATION NUMBER: 60/079664
 / PRIOR FILING DATE: 1998-03-27
 / PRIOR APPLICATION NUMBER: 60/079786
 / PRIOR FILING DATE: 1998-03-27
 / PRIOR APPLICATION NUMBER: 60/080107
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 / PRIOR APPLICATION NUMBER: 60/080194
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 / PRIOR APPLICATION NUMBER: 60/081070
 / PRIOR FILING DATE: 1998-04-08
 / PRIOR APPLICATION NUMBER: 60/081195
 / PRIOR FILING DATE: 1998-04-09
 / PRIOR APPLICATION NUMBER: 60/081838
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 / PRIOR APPLICATION NUMBER: 60/082568
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 / PRIOR FILING DATE: 1998-04-21
 / PRIOR APPLICATION NUMBER: 60/082704
 / PRIOR FILING DATE: 1998-04-22
 / PRIOR APPLICATION NUMBER: 60/082797
 / PRIOR FILING DATE: 1998-04-22
 / PRIOR APPLICATION NUMBER: 60/083322
 / PRIOR FILING DATE: 1998-04-28
 / PRIOR APPLICATION NUMBER: 60/083495
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083496
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083499
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/083559
 / PRIOR FILING DATE: 1998-04-29
 / PRIOR APPLICATION NUMBER: 60/084366
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/084414
 / PRIOR FILING DATE: 1998-05-06
 / PRIOR APPLICATION NUMBER: 60/084439
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/084640
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/084643
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/085573
 / PRIOR FILING DATE: 1998-05-07
 / PRIOR APPLICATION NUMBER: 60/085579
 / PRIOR FILING DATE: 1998-05-15
 / PRIOR APPLICATION NUMBER: 60/086023
 / PRIOR FILING DATE: 1998-05-18
 / PRIOR APPLICATION NUMBER: 60/086392
 / PRIOR FILING DATE: 1998-05-22
 / PRIOR APPLICATION NUMBER: 60/086486
 / PRIOR FILING DATE: 1998-05-22
 / PRIOR APPLICATION NUMBER: 60/087098
 / PRIOR FILING DATE: 1998-05-28
 / PRIOR APPLICATION NUMBER: 60/087208
 / PRIOR FILING DATE: 1998-05-28
 / PRIOR APPLICATION NUMBER: 60/087609
 / PRIOR FILING DATE: 1998-06-02
 / PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
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 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089518
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089653

Qy 181 LRRKSPASGGPMCNVKAPLGSPSPRRAKRFASLSPRFVETLYVADDKMAAFHGAGLKR 240
 Db 181 LRRKSPASGGPMCNVKAPLGSPSPRRAKRFASLSPRFVETLYVADDKMAAFHGAGLKR 240

Qy 241 YLTIVMAAAAKAFKHPSTRNPVSLVTRVLIGSGBGPQVPSAATLRSFCAWQRLNL 300
 Db 241 YLTIVMAAAAKAFKHPSTRNPVSLVTRVLIGSGBGPQVPSAATLRSFCAWQRLNL 300

Qy 301 TPESDPDPFDTAILFTRDLCGVSTCDTLGMADGTYCDPARSCALVEDGQSAFTAA 360
 Db 301 TPESDGPDPFDTAILFTRDLCGVSTCDTLGMADGTYCDPARSCALVEDGQSAFTAA 360

Qy 361 HEIGHTFNMHDNSKPCITSNLGPLSTSRRHMAPVMAHDPERPWSPCSARPFTDFLNGY 420
 Db 361 HEIGHTFNMHDNSKPCITSNLGPLSTSRRHMAPVMAHDPERPWSPCSARPFTDFLNGY 420

Qy 421 GRLLDKPEAPNLPVTPGKDYDADRCQLTGPDSRHCPOLPCCALWCSGHNLNGHA 480
 Db 421 GRLLDKPEAPNLPVTPGKDYDADRCQLTGPDSRHCPOLPCCALWCSGHNLNGHA 480

Qy 481 MCOTKHSWPADGTPCGPAQQACNGCRCLHMDQDFNTPQAGGNGPWPWGDSRTCGGGV 540
 Db 481 MCOTKHSWPADGTPCGPAQQACNGCRCLHMDQDFNTPQAGGNGPWPWGDSRTCGGGV 540

Qy 541 QFSSRQDCTRPRVPRNGKCYCEGRTRFRSNCNTEDCPTGSALTSPREQQAAYNHRTDLPKSF 600
 Db 541 QFSSRQDCTRPRVPRNGKCYCEGRTRFRSNCNTEDCPTGSALTSPREQQAAYNHRTDLPKSF 600

Qy 601 PGPMDWTPRTGVAPDQCKLTQARALGTYTLEPRVVDGTPCSPDSSSVCGRCIHA 660
 Db 601 PGPMDWTPRTGVAPDQCKLTQARALGTYTLEPRVVDGTPCSPDSSSVCGRCIHA 660

Qy 661 GCDRIGSKKKEDDKCKMYCGGDGSGCKSKOSGSFRKFRYGNNTVTIPAGATHILVRQOQNP 720
 Db 661 GCDRIGSKKKEDDKCKMYCGGDGSGCKSKOSGSFRKFRYGNNTVTIPAGATHILVRQOQNP 720

Qy 721 GHRSIYIALKLPLDGSVALNGEYTLMPSPDVTLLPGAVSLRSGATASETLSGHGLAQP 780
 Db 721 GHRSIYIALKLPLDGSVALNGEYTLMPSPDVTLLPGAVSLRSGATASETLSGHGLAQP 780

Qy 781 LTLQVLYAGNPDTTRLYSFFYPRPTPSTPRPTPDTWLRRAQILELRRRPWAGRK 837
 Db 781 LTLQVLYAGNPDTTRLYSFFYPRPTPSTPRPTPDTWLRRAQILELRRRPWAGRK 837

RESULT 12
 US 10-17483-352
 ; Sequence 352, Application US/10176483
 ; Publication No. US0030017541A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Godowski, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.

Qy 1 MSQTGSHHGRGLAGRMLMGQPCUPLPVLPLVPLSMVWILLASILLASPLPREE 60
 Db 1 MSQTGSHHGRGLAGRMLMGQPCUPLPVLPLVPLSMVWILLASILLASPLPREE 60

Qy 61 1VPFKLNGSVLPQSGAARLLCRLQAFGTLLBLBDSGVQVEGIFTQYQGAPPLLG 120
 Db 61 1VPFKLNGSVLPQSGAARLLCRLQAFGTLLBLBDSGVQVEGIFTQYQGAPPLLG 120

Qy 121 GASPQTYLTGTINGDPESVASHLWDGGALLGTVQYRGAELHQIPLCSTPNAGGPGAAH 180
 Db 121 GASPQTYLTGTINGDPESVASHLWDGGALLGTVQYRGAELHQIPLCSTPNAGGPGAAH 180

Qy	781	LTLQVLVAGNPQDTRLYSPFPVPRPTPSTPRPTPQDWLHRRQAILBLRRLRPWAGRK	837	Db	481	MCQTKHSPWADGTPCGPAQACMGRCLHMDQLQDFNIPQAGGWWGPNGPWGDCSRTCGGV	540
Db	781	LTLQVLVAGNPQDTRLYSPFPVPRPTPSTPRPTPQDWLHRRQAILBLRRLRPWAGRK	837	Qy	541	QFSSRQDCTRYPVRPGGKXCEGRRTFRSNCNTEDCPTGSALTFRREEQCAAYNHRTRDLPKF	600
		RESULT 14		Db	541	QFSSRQDCTRYPVRPGGKXCEGRRTFRSNCNTEDCPTGSALTFRREEQCAAYNHRTRDLPKF	600
	US-10-176-914-352	Sequence 352, Application US/10176914		Qy	601	PGPMDDNPYPRYTGVAPODQCKLTQCARALGTYYLBRVVDGTPCSDDSSVQYQGRCHIA	660
	Publication No. US20030017545A1	GENERAL INFORMATION:		Db	601	PGPMDDNPYPRYTGVAPODQCKLTQCARALGTYYLBRVVDGTPCSDDSSVQYQGRCHIA	660
		APPLICANT: Baker, Kevin P.		Qy	661	GCDRIGSKKKEDPKCMVCGDGSCKQSFRKFRYGNVNTIPAGATHILVRQGNP	720
		APPLICANT: Chen, Jian		Db	661	GCDRIGSKKKEDPKCMVCGDGSCKQSFRKFRYGNVNTIPAGATHILVRQGNP	720
		APPLICANT: Desnoyers, Luc		Qy	721	GHRSIYIALKLPDGSYALNGEYTLMPSPTDVVLPGAVSLRSGATAASETLSGHGPLAQ	780
		APPLICANT: Goddard, Audrey		Db	721	GHRSIYIALKLPDGSYALNGEYTLMPSPTDVVLPGAVSLRSGATAASETLSGHGPLAQ	780
		APPLICANT: Godowski, Paul J.		Qy	781	LTLQVLVAGNPDTTRLYSPFPVPRPSPTRPTPQDWLHRRQAILBLRRLRPWAGRK	837
		APPLICANT: Gurney, Austin L.		Db	781	LTLQVLVAGNPDTTRLYSPFPVPRPSPTRPTPQDWLHRRQAILBLRRLRPWAGRK	837
		APPLICANT: Pan, James					
		APPLICANT: Smith, Victoria					
		APPLICANT: Watanabe, Colin K.					
		APPLICANT: Wood, William I.					
		APPLICANT: Zhang, Zemin					
		TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME					
		FILE REFERENCE: P4430RIC83					
		CURRENT APPLICATION NUMBER: US/10/176, 914					
		Prior Application removed - See File Wrapper or Palm					
		NUMBER OF SEQ ID NOS: 612					
		SEQ ID NO 352					
		TYPE: PRT					
		ORGANISM: Homo Sapien					
	US-10-176-914-352	Query Match 99.8%; Score 4563; DB 14; Length 837;					
		Best Local Similarity 99.9%; Pred. No. 0;					
		Matches 836; Conservative 1; Indels 0; Gaps 0;					
Qy	1	MSQTGSHPGRGLAGRWIGAQPCILLLTVPUSWLWVLLILLASLPSARLASPLPREE	60				
Db	1	MSQTGSHPGRGLAGRWIGAQPCILLLTVPUSWLWVLLILLASLPSARLASPLPREE	60				
Qy	61	IVPEPKLNGSVLPGSGAPARLLCRLQAFGETLLELQDSGVQVEGLTVQYQVQAPBLIG	120				
Db	61	IVPEPKLNGSVLPGSGAPARLLCRLQAFGETLLELQDSGVQVEGLTVQYQVQAPBLIG	120				
Qy	61	GAEPTGYLTGTINGDPESVASHWDGALLGTVQYQGAELHQPQLEGTPNSAGGGCAHI	180				
Db	121	GAEPTGYLTGTINGDPESVASHWDGALLGTVQYQGAELHQPQLEGTPNSAGGGCAHI	180				
Qy	181	LRRKSPASQGQPMCNTVAKPGLSPSPRPRAKFASLRFVETLWVADDKMAFHAGLKR	240				
Db	181	LRRKSPASQGQPMCNTVAKPGLSPSPRPRAKFASLRFVETLWVADDKMAFHAGLKR	240				
Qy	241	YLTVMAAAAKAFKHPSTRNPVSLVTRVILGSGBGPQVQPSAAQTLSRSCAWQRLIN	300				
Db	241	YLTVMAAAAKAFKHPSTRNPVSLVTRVILGSGBGPQVQPSAAQTLSRSCAWQRLIN	300				
Qy	301	TPEDSDPDPFDIAILFTRDLCGVSTCDLGADVGTVCPDARSAIVEDDGLQSAFTAA	360				
Db	301	TPEDSDPDPFDIAILFTRDLCGVSTCDLGADVGTVCPDARSAIVEDDGLQSAFTAA	360				
Qy	361	HEIGHVNMHDNSKPCITSNCPLSTERHMAPVMAHVDPEEPWSPSARFTTDFLDNGY	420				
Db	361	HEIGHVNMHDNSKPCITSNCPLSTERHMAPVMAHVDPEEPWSPSARFTTDFLDNGY	420				
Qy	421	GHCLLDKPKRAPELHLPLVTFPKDQYDADRCQLTFGPDSRHCPCOLPPCAALWCSGHNLHGA	480				
Db	421	GHCLLDKPKRAPELHLPLVTFPKDQYDADRCQLTFGPDSRHCPCOLPPCAALWCSGHNLHGA	480				
Qy	481	MCOTKHSPWADGTPCGPAQACMGCRCLHMDQDFNTPQAGGWWGPNGPWGDCSRTCGGV	540				
Qy	481	YLTVMAAAAKFKHPSIRNPVSLVYTRVILGSGEKGPOVQPSAAQTLSRSCAWQRLIN	300				

Db 241 YLTVMARAAKAFKHPSIRNPVSLVTRVLIGSGBGPQVQPSAAQTL&FCAVQRLN 300
 Qy 301 TPEDSPDPFDTAILFTRDLCGVSTCDTLGMADVGTVCDPARSACIVEDGLQSAFTAA 360
 Db 301 TPEDSPDPFDTAILFTRDLCGVSTCDTLGMADVGTVCDPARSACIVEDGLQSAFTAA 360
 Qy 361. HELGHVPMNLHDNSKPCISLNGPLSTSRRHMAPVMAHVDPEPWSPCSARPTTIDLDNGY 420
 Db 361. HELGHVPMNLHDNSKPCISLNGPLSTSRRHMAPVMAHVDPEPWSPCSARPTTIDLDNGY 420
 Qy 421. GHCLDKPAPLHLPVTFPGDQYDADRCQLTIFGDPDRHCPOLPPAALWCSGHNLNGHA 480
 Db 421. GHCLDKPAPLHLPVTFPGDQYDADRCQLTIFGDPDRHCPOLPPAALWCSGHNLNGHA 480
 Qy 481. MCQTKHSPWADGTPCGPAAQACMGRCIHMIDOLQDNTIPOAGGGMGPWGDSCRTCGGV 540
 Db 481. MCQTKHSPWADGTPCGPAAQACMGRCIHMIDOLQDNTIPOAGGGMGPWGDSCRTCGGV 540
 Qy 541 QFSSRDCTPVPANGKCYCEGRTRFRSNTCECPTGSALTRREBOAAYNHRTDLFKSF 600
 Db 541 QFSSRDCTPVPVRNGKCYCEGRTRFRSNTCECPTGSALTRREBOAAYNHRTDLFKSF 600
 Qy 601 PGPMDWVPRYTGVAPODQCKLTCARALGYYTLEPRVTDGFCSPDSSSVCVQGRCIHA 660
 Db 601 PGPMDWVPRYTGVAPODQCKLTCARALGYYTLEPRVTDGFCSPDSSSVCVQGRCIHA 660
 Qy 661 GCDRTIGSKCKFDKCMVCGDGSCKSKQGSFRYGNVVTIPAGATHILVRQGNP 720
 Db 661 GCDRTIGSKCKFDKCMVCGDGSCKSKQGSFRYGNVVTIPAGATHILVRQGNP 720
 Qy 721 GHRSTYLAKLKDPSYALNGBEYTLMPSPTDVVLPGAVSLRYSGATAASETLSGHGLAQ 780
 Db 721 GHRSTYLAKLKDPSYALNGBEYTLMPSPTDVVLPGAVSLRYSGATAASETLSGHGLAQ 780
 Qy 781 LTLOVLYAGNPQDTLRYSEFVPRPTPSPRPTQDMLIRRAQILEILRRPWAAGRK 837
 Db 781 LTLOVLYAGNPQDTLRYSEFVPRPTPSPRPTQDMLIRRAQILEILRRPWAAGRK 837

Search completed: April 1, 2005, 12:45:18
 Job time : 153 secs

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Om protein - protein search, using sw model

Run on: April 1, 2005, 12:42:07 ; Search time 51 Seconds
 1579.087 Million cell updates/sec (without alignments)

Title: US-09-634-287B-2

Perfect score: 4570

Sequence: 1 MSQTGSHPGRGLAGRWLNGA.....LHRRAQILBILRRPWRAGRK 837

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% ; Maximum Match 100%

Listing First 45 summaries

Database : PIR 79/*
 1: Pirl: *
 2: Pir2: *
 3: Pir3: *
 4: Pir4: *

RESULT 1
 T00355 hypothetical protein KIAA0688 - human
 C;Species: Homo sapiens (man)
 C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
 C;Accession: T00355
 R:Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Nomura, N.,
 DNA Res. 5, 169-176, 1998
 A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete
 A;Reference number: Z14142; MNUD:98403880; PMID:9734811
 A;Accession: T00355
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Cross-references: UNIPROT:075173; EMBL:AB014588; NID:93327189; PIDN:BA31663.1; PID:93:
 A;Experimental source: brain
 A;Genes: KIAA0688
 P;519-575/Domain: thrombospondin type 1 repeat homology <THR3>

Query Match 99.9%; Score 4566; DB 2; Length 837;
 Best Local Similarity 99.9%; Pred. No. 1.8e-302;
 Matches 836; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSQTGSHPGRGLAGRWLNGAQCPLIPLIVPLISWLWMLLILASLPLSPRREE 60
 Db 1 MSQTGSHPGRGLAGRWLNGAQCPLIPLIVPLISWLWMLLILASLPLSPRREE 60
 Qy 61 IYPPPEKLNGSLVLPGSGAPARLICRQAFGETLLEEQDGSQYQVEGLTVQYLGQAPLLG 120
 Db 61 IVFPEKLNGSLVLPGSTPAPLICRQAFGETLLEEQDGSQYQVEGLTVQYLGQAPLLG 120
 Qy 121 GAEPGTYLTGTGTINGDPESVASHLWDGALLQYQGAEHLQPLLEGTPNSAGGPQAH 180
 Db 121 GAEPGTYLTGTGTINGDPESVASHLWDGALLQYQGAEHLQPLLEGTPNSAGGPQAH 180
 Qy 181 LRRKSPASQGGMCNTRKAPLGSPPSPRRAKRFASTLSRFVETLVAADDKMAAFHGGLKR 240
 Db 181 LRRKSPASQGGMCNTRKAPLGSPPSPRRAKRFASTLSRFVETLVAADDKMAAFHGGLKR 240
 Qy 241 YLTIVMAAAAKAFKPHPSIRNPVSLVTVRLVILGSGEGPQGPSAAQTLRSFCAWQGLN 300
 Db 241 YLTIVMAAAAKAFKPHPSIRNPVSLVTVRLVILGSGEGPQGPSAAQTLRSFCAWQGLN 300
 Qy 301 TPBDSPPDHFTDIALPTRDLCGVSCTDLCGMADYTVCDPARSCLAEVDDCLQSATAA 360
 Db 301 TPBDSPPDHFTDIALPTRDLCGVSCTDLCGMADYTVCDPARSCLAEVDDCLQSATAA 360
 Qy 361 HELGHVNMLHDNSKPCISLNGPLSTSRSRHYMAPVMAHVDPEEPWPSOSARFTTDFLNGY 420
 Db 361 HELGHVNMLHDNSKPCISLNGPLSTSRSRHYMAPVMAHVDPEEPWPSOSARFTTDFLNGY 420

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4566	99.9	837	2 T00355	hypothetical protein hypothetical prote gene ADAMTS-1 prot hypothetical prote hypothetical prote procollagen N-prope protein C3/C3.6a [hypothetical prote angiogenesis inhib hypothetical prote hypothetical prote meltrin alpha - mo hypothetical prote catrocollaratin P disintegrin-like m ecarin precursor thrombospondin 1 P hypothetical prote thrombospondin 1 P jarathagin C precu trigramin precursor thrombospondin pre atroslysin A (EC 3. atroslysin B (EC 3. vascular apoptosis metalloproteinase metalloproteinase monocyte surface a thrombospondin 2 P fibrinolytic metal
2	2158	47.2	951	2 T00017	
3	1755.5	30.1	550	2 T47158	
4	1317	28.8	2165	2 T21371	
5	950.5	20.8	1205	2 T18517	
6	480.5	10.5	1558	2 C89114	
7	480.5	10.5	2167	2 T3395	
8	415.5	9.1	1444	2 T18856	
9	389	8.5	860	2 T18892	
10	365	8.0	951	2 T00460	
11	313	6.8	903	2 S60257	
12	284.5	6.2	957	2 T15976	
13	268.5	5.9	609	2 S55270	
14	268.5	5.9	814	2 G02390	
15	267	5.8	616	2 A55796	
16	266.5	5.8	1170	1 TSHD01	
17	263.5	5.8	1059	2 T22545	
18	263	5.8	1170	2 A40558	
19	26.0	5.7	571	2 S24789	
20	25.3	5.5	480	1 A30065	
21	25.1	5.5	1178	1 A32904	
22	25.0	5.5	419	2 S41607	
23	24.3	5.3	478	2 A42296	
24	24.1	5.3	610	2 JC7530	
25	23.9.5	5.2	407	2 S66260	
26	23.9.5	5.2	549	2 A49169	
27	23.7.5	5.2	826	2 A60385	
28	23.7.5	5.2	1172	1 TSHD02	
29	235.5	5.2	478	2 JC4880	

Qy	421 GHCLDKPAPLPHLPVTPGKDYDADRCQLTGFPPDSRHKPQLPPCAALWCSHLNHA	480	284 SAAOTLRSFCAWQGLNTPEDSPDHFTDAILFTRODLCGVSTCDTIGMADYGTVCDDP 343	
Db	421 GHLLDREPAHLPLPVTGKDYDADRCQLTGFPPDSRHKPQLPPCAALWCSHLNHA	480	308 NAALTIRNFCNWKQHNPSDRDEHDTAILFTRODLCGVSTCDTIGMADYGTVCDDP 367	
Qy	481 MCOTKHSKPWADSTPGPAAQACMGCRCLHMDOLODFNTIPQAGGWGPMPGDPCSRQCGGV	540	344 SCA1VEDDLOSAFTAAHELGHYFVNMLHDNSKPCISLNGPLSTSRYMAPYMAHVDPEEP 403	
Db	481 MCOTKHSKPWADGTPGPAQACMGCRCLHMDOLODFNTIPQAGGWGPMPGDPCSRQCGGV	540	368 SCSVIEDDGIQAAATTAAHELGHYFVNMPHDAXHCASTINGVTGDS-HMASMLSLDSQP 426	
Qy	541 QFSSRDTCTRIPVRPGRGKCYCEGERTRTRFSNTEDCPGSSALTFREBQAAANHRTDLFKSF	600	404 WSPCSARFPTTDLFGYGHCLLQKPEAPLPHLPVTPGKDYDADRCQLTGFPPDSRHKPQL 463	
Db	541 QFSSRDTCTRIPVRPGRGKCYCEGERTRTRFSNTEDCPGSSALTFREBQAAANHRTDLFKSF	600	427 WSPCSAYMTSFLDNGHGBCLMDKPKQNPKLPSDLPGLYDANRQCCPTFGEBSKHCDDA 486	
Qy	601 PGPMNDWVPRYTGVAPODCKLTCQARALGTTYLEPRVVDGTPCSPDSSSVCYQGRCIHA	660	464 PPPCAALWCSGHLMCHAMCOTKHSIPWADGTPCSPGAQACMGCRCLHMDOLODFNTIPQAGGW 523	
Db	601 PGPMNDWVPRYTGVAPODCKLTCQARALGTTYLEPRVVDGTPCSPDSSSVCYQGRCIHA	660	487 ASTCPTLWCGTGSLLVQTKHFWADOTSCSGEGKWCYSGKCVNKTDMKHFATPVNQSSW 546	
Qy	661 GCDRIIGSKKFKDCKMVGCGDGGCSKOSGSFPRKFYRGGNNVTTIPAGATHILVRQGNP	720	524 GPWGPWGDCSRTICGGQFQFSRSDCTRPVPRNGGKCYCEGRTRTRFSNTEDCPGSSALFPR 583	
Db	661 GCDRIIGSKKFKDCKMVGCGDGGCSKOSGSFPRKFYRGGNNVTTIPAGATHILVRQGNP	720	547 GPWGPWGDCSRTICGGQFQTMRECDNPVPRNGGKCYCEGRTRTRFSNTEDCPDNGKTFPR 606	
Qy	721 GHRSIYLAALKLPLDPSYALNGEYTLMPSPDVTWPLGAVSLRYGATASETLSGHGPLAQ	780	584 BEQCAHYNHTDLFKSFPGPMDWVPRYTGVAPODCKLTCQARALGTTYLEPRVVDGTP 643	
Db	721 GHRSIYLAALKLPLDPSYALNGEYTLMPSPDVTWPLGAVSLRYGATASETLSGHGPLAQ	780	607 EEQCEAHNEFESKASFGNEPTWVTPKAGVSPKDRCKLTCEARQGIVYFPLQPKVVDGTP 666	
Qy	781 LTLOQTVLVAQNPDQTRLRYAFFVPRPRTPSTSPRPTQDWLHRAAQILETRRREWAGRK	837	644 CSPDSSSVCYQGRCHAGCDR115SKKEDKCMVYCGDGGCSKOSGSFPRKFYRGGNNVY 703	
Db	781 LTLOQTVLVAQNPDQTRLRYAFFVPRPRTPSTSPRPTQDWLHRAAQILETRRREWAGRK	837	667 CSPDSSSVCYQGCTKAGCDR115SKKEDKCMVYCGDGGCSKOSGSFPRKFYRGGNNVY 726	
Qy	727 TIPAGATHILYRQOQNGHRS--IYALAKLPLDGSYALNGEYTLMPSTDVVLGRAVSLRY	761	704 TIPAGATHILYRQOQNGHRS--IYALAKLPLDGSYALNGEYTLMPSTDVVLGRAVSLRY 761	
Db	727 TIPAGATHILYRQOQNGHRS--IYALAKLPLDGSYALNGEYTLMPSTDVVLGRAVSLRY	761	727 TIPAGATHILYRQOQNGHRS--IYALAKLPLDGSYALNGEYTLMPSTDVVLGRAVSLRY 785	
Qy	762 SGATASSETLSGHGPLAQPTLQVNTVAGNFOQDTRLRYSPFVPRPRTS-TPRPTQDWL	818	762 SGATASSETLSGHGPLAQPTLQVNTVAGNFOQDTRLRYSPFVPRPRTS-TPRPTQDWL 818	
Db	786 SGSSAALERTRTSFSPLKEPLIQVLMVGHALRPKTFYFMKKKTESENAILPTFSEWV	843	786 SGSSAALERTRTSFSPLKEPLIQVLMVGHALRPKTFYFMKKKTESENAILPTFSEWV 843	
RESULT 3				
T00017	gene ADAMTS-1 protein - mouse		T47158 hypothetical protein DKFZp762C110.1 - human (fragment)	
C;Species: Mus musculus (house mouse)		C;Species: Homo sapiens (man)		
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 15-Mar-2004		C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004		
C;Accession: T0017		C;Accession: T47158		
R;Kano, K.; Lizasa, H.; Ohno, S.; Matsushima, K.		R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Weil, B.; Wiemann, S.		
A;Title: The exon/intron organization and chromosomal mapping of the mouse ADAMTS-1 gene		A;Submitted to the Protein Sequence Database, March 2000		
A;Reference number: Z14055; PMID: 98110583; PMID: 9441751		A;Reference number: Z224379		
A;Accession: T0017		A;Accession: T47158		
A;Status: preliminary; translated from GB/EMBL/DBJ		A;Cross-references: UNIPROT:Q9H1H8; EMBL:AI162080		
A;Molecule type: DNA		A;Experimental source: adult melanoma (HeLa cell line); clone DKFZp762C110.1		
A;Residues: 1-551 <HR>		C;Genetics:		
A;Cross-references: EMBL:AB001735; NID: 92809056; PID: BAA24501.1; PID: g2809057		A;Note: DKFZp762C110.1		
C;Genetics:		Query Match 30.1%; Score 1375.5; DB 2; Length 550;		
A;Gene: ADAMTS-1		Best Local Similarity 54.3%; Pred. No. 86-86; Mismatches 1.8; Gaps 6;		
A;Introns: 1-51 <HR>		Matches 241; Conservative 78; Mismatches 7; Gaps 6;		
F;542-598; Domain: thrombospondin type 1 repeat homology <THR3>		2 SLLG-VNQDSHMMASLNSQWSPCSAYMTISFLDNGHGECLMDKPNQNP1QLPGDL 60		
Query Match 47.2%; Score 2158; DB 2; Length 951; Best Local Similarity 49.4%; Pred. No. 1e-118; Mismatches 135; Conservative 414; Matches 414; Mismatches 221; Indels 68; Gaps 16;		379 SINGPLSTSRYMAPYMAHVDPEEPSPCSARFIDFLDNGYGHCLLDKPEAFLHLPVTF 438		
Db	37 LILLIAS--LIPSARIA--SPLPRREEVYPEKINGSVLPGSGAPARLICRLOAEGTL 92	18 MLLLAASTTMILCARAAGTREEDEVLYPSLERA--PGHDESTTRL-RUDAFGQL 73	Db	439 PGKDYDADRCQLTGFPSRHCQPLPPCAALWCSHLNHAQHLDPTGDLAHCYSGCTVNGDPCSAAL 129
Qy	93 LLIELEQDSGVQEVGLTVQYLGQAPELLGAE-----PGTYLTGTTINGDPESVSL 142	74 HUKLQPDSSGFLPLAFGPTILQTVGRSP---GSEAQHLDPTGDLAHCYSGCTVNGDPCSAAL 129	Db	61 PGTSYDANRQCCPTFGEDESKHCFCDAASTCSTLWCTGSGVLLVQTKHFPWADGTSCEG 120
Db	130 SLCBEG-VRGAFYLVQGEEBFPIQAPGATLRLAPAVDEESSARPQFHILRRRGSG-CA 187	143 HWDGGALLGVQYRGAAHLQPLEG-----GTP-NSAGGPGAHILRLRKSPASGQGP 192	Qy	499 QACMGCRCLHMDOLODFNTIPQAGGWGPWGDGCSRTCGGVQFSRSDCTRPPRNGK 558
Qy	193 MCNIV-----KAPLGSPSPRPR-----RAKRFASLSRFVETL 223	188 KCQCMYMDDETLPTSDSRPSQNTRNQVDRPQDAGKPSGPGSIRKRFVSSPRVETM 247	Db	121 KWCINGKCVNKTDEKHFDTPHGSGWGMGPWDGCSRTGGQYQTMRECDNPYPKNGK 180
Db	188 KCQCMYMDDETLPTSDSRPSQNTRNQVDRPQDAGKPSGPGSIRKRFVSSPRVETM 247	248 LVDQSMWDFHGSGLKEYLTLTFSVAAFRYKHPStIRNISIsvvKKLIVYBEQKGPEVTS 307	Qy	559 CEGRRTRFRSCNTEDCPGSSALTFREEQCAAYNHRIDL-FKSFPGPMWVPRYTGVAQFD 617

Db	161	CEGKRVYRSCNLEDCPDNGKTFREEQBAHNEBPSKASFGSGP-A-VEWPKAGVSPKD	239	Qy	379	SLNGLPLS-----TSRHMAPMAYDPEEPWSPCSARFITDFLDNGYG- 421
Qy	618	OCKLTGCGARALGYYYLEPRYVDGTPCSPDSSVYQGRCTHAGCDRIGSEKKEKDCMV	677	Db	441	STYMPNPKVCFQSTKEKDQFQNNFIMAPLEYNATHPWSMSPCAGMLBREFLENRNGQ 500
Db	240	RCKLICQKIGIGFFVYLOPKWVQDGTPCSPDSTSVCQGQVKAGCDRINDSCKKFDKGV	299	Qy	422	-HCLLDKPEAHLHLPPTF----PGKDYDADRCQLTGPDSHRCPPQDPPCAALWCGHL 476
Qy	678	CGDGSGCSKQSSSFRKRYGIANVVTIPIAGATHILVRQGNPGRHS--IYIALKUPDGS	735	Db	501	TOCLFLDOPVERRYEYDFVRLDEPKYCDAHQCKFVGPASELCPM- PTCCRILWCATPY 559
Db	300	CGNGSTCKKISSESVTSAKPGYHDIIITPTGATNIEVKRNQGSRNSRNGSFLAIAKDT	359	Qy	477	NGHAMCOTKHSKPHADGTPCGPAOA--CMGGRCIHLMDQDFTNPOA----GGWGPNGPW 529
Qy	736	YALNGETTLMSPSTDWVLPGAVSLRYSGATASETLSGHSGLAQPPLTQLQVLAGNPDT	795	Db	560	GSQMGCKTQHMEWADGTPCDBERSMSPFHHGACVRL----APESLTKIDCQWGDWRSW 612
Db	360	YIINGDTIYSTLEQDINYKGVV-LRYSSSAALERIRRSPLXPLTQVLTGVNALRPK	418	Qy	530	GDCCSRGGYQFSSSDCTRTPRNGSKYCEGRTRTFRPSCNTEDCPNGSALTFRBECQAA 589
Qy	796	LYSFYFVRPTPS-TPRPTPQDWL 818		Db	613	GECCSRGGYQGKLRCDSPKPRNGSKYCEGRTRTFRPSCNTEDCPNGSALTFRBECQAA 671
Db	419	IKTYFVKKCESFNAIPTFSAMV 442		Qy	590	YNHRTDIFKSFQGP-MDWVPRYTGVAQDQCKLTQARALGYYVLEPRVVDGTPCPSPDS 648
Db				Db	672	ENNKDGIQGYASTNTWVPCYANVAPNERNCKLYCRLSGSAAFYLRLRKVDDGTPCDRNG 731
RESULT 4						
T21371		hypothetical protein F25H8.3 - Ceanorhabditis elegans		Qy	649	SSVCVGCRCTHAGCDRITGSKCKFDKMVGCGDGSCKSKQGSCF-RKFRYGNVNVVTPA 707
C;Species:	Ceanorhabditis elegans			Db	732	DDICVAGACMAGCDHLSHTRRDKGVCDDSSCKVKGTFNNEGFTGNEVMKIPA 791
C;Accession:	T21371; T24896			Qy	708	GATHILVROQG--NPGRHSRIVYLALKLPGDSYALNGEYTLMPSPSTDVULPGAVSLRSGAT 765
R;Gajadhy, S.				Db	792	GSANIDIRQKGNNMEDDNTYLSLRANGEFBLNGFQVSALARQQAFAQDFTV-LESGSD 850
submitted to the EMBL Data Library, February 1996				Qy	766	ASETTSQGHGLAQPPLTQLVL-VAGNPQDTRLY 798
A;Reference number: Z19413				Db	851	AITERINGTGPTRSDIYVHVLVSGSPHPDISYBY 884
A;Accession: T21371						
A;Status: preliminary; translated from GB/EMBL/DDBJ						
A;Molecule type: DNA						
A;Residues: 1-2165 <WIL>						
A;Cross-references: UNIPROT:Q11791; EMBL:Z69360; PIDN:CAA93287.1; GSPDB:GN00022; CESP:F2						
A;Experimental source: R;Gajadhy, S.						
submitted to the EMBL Data Library, February 1996						
A;Reference number: 219499						
A;Accession: T24896						
A;Status: preliminary; translated from GB/EMBL/DDBJ						
A;Molecule type: DNA						
A;Residues: 1-2165 <WIL>						
A;Cross-references: EMBL:269361; PIDN:CAA93288.1; GSPDB:GN00022; CESP:F25H8.3						
A;Experimental source: clone T13H10						
C;Genetics:						
A;Gene: CESP:F25H8.3						
A;Map Position: 4						
A;Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 495/2; 547/3; 584/3; 634/2; 744/1; 81						
Matches 280; Best Local Similarity 37.1%; Score 1317; DB 2; Length 2165;						
Qy	109	YQVLGQAPBLIGG---AEGPTYLTGTG-----DPVSVAHLWDGAGLUGVLRGAEHLQP	164	Db	149	VLYDSEEEVRGCGMSRTDPDCIYRAHVKVHOHSIVNLCDSEDGLYGMLALPSGIHTEP 208
Matches 280; Best Local Similarity 37.1%; Score 1317; DB 2; Length 2165;						
Qy	165	LEGTGTPNSAGGGP---AHLIREKSP-----ASGGFEMCNVYKAPL 200	264	Db	209	1ISGNGTEHDGASRHRORLVRKEPDMPHIFKSFQHNLSTSVNETETTATWQDOWEDY-----
Db	201	GSPSPRPRAKRFA-SLSRFEVETLVVADDKMAAFAHFGGLKRYYLITMAAAAKAKAKHPSIR	259	Qy	265	--IERTKARSRAAANSWHDHYYEVVWVADTKNTEYHGRSLSEDYVLTFLSTVASYRQSLR 321
Qy				Db		NPVSLVYTRVLVILGSGBGPQVGPSSAQLTREPCAWORGTLATPESDSDPHDPTAILEFTRQ 319
Db				Qy	260	ASINVVVVYLKTEENAPRITONAQTLQDFCRWQOYNDPDDSSVQHHDVAILITRK 381
Qy				Db		DIC-GVSTCDTGMADYGTWCDPARSAAVEDGLQSAFTAAHELGHVFMMLHDNEKPC1 378
Db				Qy	320	DICRSQGKCDTGLAELGQVYRGAELHLQPLEGGTPNSAGCPG-AHILRKSKPASQGMCNVK 197
Qy				Db		107 VFGRDHLRLPNARLVAAGTAVWQES---GATRVEPLLTGCLYVGDAGLAEASSS 161

Db	162 VAIISNCDS- -LQOLIRMEEEFPIEPLKGLAAKEAQHRYVYHR- PITSRPP-----213	Qy 519 QAGGWWGPWGPGPWSRCDTFRSNTEDCPTGS 578
Db	198 APLGSP-----SPPRRAKRFASLISRFTETLVVADDKM 230	Db 75 ETGNGWPVPPENCSRSQGGVQLERQCSGD-----CTGASTRYISCNLACEST 126
Qy	199 : : : : : : : : : : : : :	Qy 579 ALTFREQQCAAYNHRDILFKSFPGPMD-----WVPRITGVAPQDOCKLTQARALGYYV 633
Db	214 -PLGGPQALDTGISADSIDSLSRALGYLTERVNSSRMRRHAAADDYNEEVLLGVDDSV 272	Db 127 -DRAEAOCSKFNDEA-----LGDNYHHRWTP-TKG-- KNKCLVCRPESGNYYK 171
Qy	221 AATFGA-GLKRYLITMBAAAKAKPHPSRINPVSLVYTRVLGLSGEEGP- -QVGPSAAQ 287	Qy 634 LEPPRVDTCPSPDSSVYQGRCHIAGCDRIGSKKKFDRKCMVCGDGSCKSGSF- 692
Db	273 VQFHGTERVQYKUHLMVNEYHDSLSGAHINVVLVRLIISLCKSMSLIEG-NPSQ 331	Db 172 WADKVYDGTCKCDSKNSNDICVCDGECLPVCDGKLGSKSKPDKCCKDGTCTKTBGRFD 231
Qy	288 TLRSCFMQORGANTPEPDSDPHDFTAILFTRODLCGYSTCDTGLMADVGTVCDPARSCL 347	Qy 693 -RKFRYGTANVVVTLIAGATHILYRQGNGPGRHSIYLAALKLPDGSYANAGEYTLIMPSTDV 751
Db	332 SLENVCRAYALQQPKDUTDHEYHDA-FLTRTDFB-GPSGMQ- -GYAFTVTCNHPVRSCTL 388	Db 232 ERNISPGHFDIILKIPEGATNIKQEARAKSTNN--LAALKNSDHFYLNGN-GLIQUVEREV 287
Qy	348 VEDDGQLSQAFTAARHELGHVFNMLHD- -NSKPCITSLNGPLSLSTSRRHMAPVMAHVDPPEPWSP 406	Qy 752 VLPGAVSLRYSGATAASETLSGHGPLAOFPLTLOVLYAGNPQDTTRLRSFVFP 803
Db	389 NHEQFSSPFVVAHETGHVYMEHDGQCNRC---GDEVRVLGSIMAPLVOAAFHREHWRSR 444	Db 288 EVGGTI-- FVYDDAEPETLSAQGPLSHEETLVALLFKGSRDTAIVYEFSSIP 336
Qy	407 CSARFITDLDNGYGHCLDCKP-- -EARLHLHPVTFPGKDYDADRCQCOLTGFPSRHCQL 463	RESULT 7
Db	445 CSQOBLSRL-HSY-DCURDDPFTHDWPA-LP-QLPGIHLHSSNEOCRFDFGJGYMMCTAF 500	T34395
Qy	464 P- -PPCAAHLWCSGHUNGHAMCOTKHSPPADGTPCGPAQACMGGRCLHM- -DLOLDNTPQ 519	C;Species: Caenorhabditis elegans
Db	501 RTFDECKQWMS- -RFDNPYFCKTKGPPDQGTMCAPGKHFQHCIVLNLTPDILK---R 554	C;Date: 29-Oct-1999 #text_change 09-Jul-2004
Qy	520 AGGKGPWGPGWGDGCSRTCGGVQFQSSRDRCDTRPVPRNGGKYCEGRRTRFRSNTEDCPTGS 579	C;Accession: T34395; T34394
Db	555 DGNNGAWSPTGSCSRTCGTGTGKFKTRQDNPHPANGRTCSGLAYDQLCNSQDCPDAAL 614	R;Geisel, C.; Bradshaw, H.
Qy	580 LTFRFREBQCAAYNHRDIL- -FKSGFPGPMDWTPRYGVAPQDOCKLTQARALGYYVLEPRV 638	A;Description: The sequence of C. elegans cosmid C37C3.
Db	615 -DFRBEQCRQW---DLYFEHGDQAHQHWTLPHEIRDA- -KERCHLYCESKETGEVVSMRMV 668	A;Reference number: Z221518
Qy	639 VDGTPCS- -PDSSSVYQGRCHIAGCDRIGSKKKFDKCMVCGDGSCKSGSFKPF- 695	A;Status: Preliminary; translated from GB/EMBL/DDBJ
Db	669 HDGTRCSYKDFASLICVRGDKCRKVQGTVGSSKQEDKCCGVCVGDINSNHKVVKGTSFSSPK 728	A;Status: Preliminary; translated from GB/EMBL/DDBJ
Qy	696 RYGGYNNVVITPAGATHILYRQGNGPGRHSIYLAALKLPDGSYANAGEYTLIMPSTDVLP 754	A;Molecule type: DNA
Db	729 KLGYKRMPEFAGARHLLIQEADITSH-- HLAQNLTETGKPLINNEENDVDPNSKTFAM 785	A;Residues: 1-155; 'SKP' <GE2>
Qy	755 GAVSLRYSGATAASETLSGHGPLAOFPLTLOVLYAGNPQDTTRLRSFVFP 802	A;Cross-references: UNIPROT:U64840; PIDN: AAC25866.1; GSPDB: GN00023; CESP: C37C3.6a
Db	786 G- -VNEYRDED-GRETLQTMGPLHETITVNPEDAR- -ISLTYKMI 830	A;Experimental source: strain Bristol N2; clone C37C3
RESUL	6	A;Accession: C37C3.6b; CESP: C37C3.6a
C99114	protein C37C3.6a [imported] - Caenorhabditis elegans	A;Map Position: 5
	C;Species: Caenorhabditis elegans	A;Introns: 32/3; 104/2; 207/1; 459/2; 536/3; 577/2; 1105/3; 1367/1; 1438/1; 1556/1
	C;Date: 10-May-2001 #text_change 10-May-2001	Query Match 10.5%; Score 480.5; DB 2; Length 2167;
	C;Anonymous: The C. elegans Sequencing Consortium.	Best Local Similarity 35.6%; Pred. No. 2.7e-24; Mismatches 46; Indels 37; Gaps 10;
	Science 282, 2012-2018, 1998	Matches 104; Conservative 46; Mismatches 105; Indels 37; Gaps 10;
	A;Title: Genome Sequence of the nematode C. elegans: a Platform for investigating biological	519 QAGGWWGPWGPGPWSRCDTFRSNTEDCPTGS 578
	A;Reference number: A75000; PMID:95069613; PMID:9851916	Db 75 ETGNGWPVPPENCSRSRQGGRHSIYLAALKLPDGSYANAGEYTLIMPSTDV 751
	A;Note: see websites genome.wustl.edu/gsc/ and www.sanger.ac.uk/Projects/C_elegans/ and www.Science 283, 35, 1999; Science 283, 2103, 1999; and	127 -DRAEAOCSKFNDEA-----LGDNYHHRWTP-TKG-- KNKCLVCRPESGNYYK 171
	A;Accession: C89114	634 LEPPRVDTCPSPDSSVYQGRCHIAGCDRIGSKKKFDRKCMVCGDGSCKSGSF- 692
	A;Status: Preliminary	172 WADKVYDGTCKCDSKNSNDICVCDGECLPVCDGKLGSLSRKFDGKCDGTCTKTBGRFD 231
	A;Molecule type: DNA	693 -RKFRYGTANVVVTLIAGATHILYRQGNGPGRHSIYLAALKLPDGSYANAGEYTLIMPSTDV 751
	A;Residues: 1-1558 <STO>	232 ERNISPGHFDIILKIPEGATNIKQEARAKSTNN--LAALKNSDHFYLNGN-GLIQUVEREV 287
	C;Cross-references: UNIPROT:Q81710; GB:chr_V; PIDN: AAC25867.1; GSPDB: GN00023	288 EVGGTI-- FVYDDAEPETLSAQGPLSHEETLVALLFKGSRDTAIVYEFSSIP 336
	A;Genetics:	
	A;Gene: C37C3.6a	
	A;Map position: 5	
Query Match 10.5%; Score 480.5; DB 2; Length 1558;		
Best Local Similarity 35.6%; Pred. No. 1.9e-24; Mismatches 46; Indels 37; Gaps 10;		
Matches 104; Conservative 46; Mismatches 105; Indels 37; Gaps 10;		

RESULT 8										
T18856	angiogenesis inhibitor homolog - Caenorhabditis elegans									
C;Species: Caenorhabditis elegans	A;Description: The sequence of <i>C. elegans</i> cosmid T19D2.									
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004										
C;Accession: T18856 ; T24653	A;Accession: T18856 ; T24653									
R;McMurray, A.	Submitted to the EMBL Data Library, July 1995									
A;Reference number: Z1.9031	A;Reference number: Z1.9031									
A;Accession: T18856	A;Status: preliminary; translated from GB/EMBL/DBJ									
A;Molecule type: DNA	A;Accession: T16692									
A;Cross-references: UNIPROT:Q8MYM8 ; EMBL:250004 ; PIDN:CAA90293.1 ; GSPDB:GN00028 ; CESP:CO	A;Status: preliminary; translated from GB/EMBL/DBJ									
A;Residues: 1-1444 <WIL>	A;Molecule type: DNA									
A;Cross-references: UNIPROT:Q8MYM8 ; EMBL:250004 ; PIDN:CAA90293.1 ; GSPDB:GN00028 ; CESP:CO	A;Accession: T18856									
A;Experimental source: clone C02B4	A;Status: preliminary; translated from GB/EMBL/DBJ									
R;McMurray, A.	Submitted to the EMBL Data Library, July 1995									
A;Reference number: Z1.9117	A;Accession: T24653									
A;Status: preliminary; translated from GB/EMBL/DBJ	A;Status: preliminary; translated from GB/EMBL/DBJ									
A;Residues: 1-1444 <WIL>	A;Molecule type: DNA									
A;Cross-references: EMBL:Z50006 ; PIDN:CAA90302.1 ; GSPDB:GN00028 ; CESP:CO2B4.1	A;Accession: T18856									
A;Experimental source: clone T07C5	A;Experimental source: clone T07C5									
A;Genetics:	A;Genetics:									
A;Map position: X	A;Map position: X									
A;Introns: 25/3 ; 70/3 ; 96/3 ; 139/3 ; 187/1 ; 234/2 ; 282/3 ; 376/2 ; 422/2 ; 478/3 ; 509/3 ; 566	A;Introns: 25/3 ; 70/3 ; 96/3 ; 139/3 ; 187/1 ; 234/2 ; 282/3 ; 376/2 ; 422/2 ; 478/3 ; 509/3 ; 566									
Query Match	Query Match									
Best Local Similarity 9.1%	Score 415.5 ; DB 2 ; Length 1444 ;									
Matches 134 ; Conservative 56 ; Mismatches 161 ; Indels 127 ; Gaps 26 ;	Pred. No. 4.5e-20 ;									
Qy	PSAAQT-----LRSPLNSCAORGQNTPEP-SDPDPHFDIALETFRQDLGVSTCDTL 330									
Db	PSALSTGVRHNGQAQSLIJDAFCYQAHNMNGPTDLMNHYDGVLIQYDHYTHTT-SVA 340									
Qy	GMADVGTVQDOPARSACIYEDDGLOSAFTPAAHELGHVFMILHD----NSKPC1-SLNG 382									
Db	341 GVAPVARNCDPLPPLPPCAFLPLPSLVEGLHGRSFVLAHEHGNMCMVHDGIVQNCNKGCCLMSAVNG 400									
Qy	PIJTSRHYMAPVMAHVDPDPEPPSPCSARFIDFL---DNGYGHCLIDKPEAPL--HL 434									
Db	401 AGKTT-----MSDCS/TREFAFLQDOLQDGLRASPLGLISTNHL 444									
Qy	PVTFPGKIDYADPQCOLTGFDPDR----HCPQLPPLPPCAFLPLPSLVEGLHGRSFVLAHEHGNMCMVHDGIVQNCNKGCCLMSAVNG 490									
Db	445 DLPLPGQRTFADQCSYFWGRDYKVEIENGRMDICRILWCG---NSGSTDSTAHL-PAL 500									
Qy	491 DGTGCGPAQAOACMGGRCLHMQLQDFN---IPOQAGGWPGW-----PGNDSGSRTECGGGVQ 541									
Db	501 EGGMCGANKWCHKGQCTHW---TFLGTTPVPTDGEWNGGAERKGCTQCAVSGSTVQ 556									
Qy	542 FSSRDCTRPVPRNGGKTCGEGRTRPRFCNTEDPTGSAITLFRREEQ---CAAYN---HR 593									
Db	557 GQRDCTVNPAPNGGKTCGEGANTRGIVCG---ATSSNCGLFTREFGNKKCISIYDPHK 613									
Qy	594 TDLFKSPFGPMDFWPRVYGV---PQDQCKLTCQ----ARALGYYVYLBPRVWQDTC 644									
Db	614 PD-----QQLTGBGFPEHSTQDPRWHLISSELRNKGQF----PDGTPC 654									
Qy	645 SPDSSVVCYQGRCTHAGCD-----RIIGSK----KKEFDKCMY-CGGDG 682									
Db	655 GFD-----AYCVGQGQCLIALSKALVQEPCDPRLEGRSVHQNWEWSSNSECSVSGCILG 710									
RESULT 9										
T16892	hypothetical protein T19D2.1 - Caenorhabditis elegans									
C;Species: Caenorhabditis elegans	C;Species: Caenorhabditis elegans									
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004	C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004									
C;Accession: T16892	C;Accession: T16892									
R;Bentley, D.	R;Bentley, D.									
submitted to the EMBL Data Library, December 1995	submitted to the EMBL Data Library, December 1995									
A;Reference number: Z18599	A;Reference number: Z18599									
A;Accession: T16692	A;Accession: T16692									
A;Molecule type: DNA	A;Molecule type: DNA									
A;Residues: 1-860 <BEN>	A;Residues: 1-860 <BEN>									
A;Cross-references: UNIPROT:Q22580 ; EMBL:U42846 ; PIDN:AAA8366	A;Cross-references: UNIPROT:Q22580 ; EMBL:U42846 ; PIDN:AAA8366									
C;Genetics:	C;Genetics:									
A;Gene: CESP:T19D2.1	A;Gene: CESP:T19D2.1									
A;Introns: 56/3 ; 96/1 ; 171/3 ; 199/3 ; 245/2 ; 293/2 ; 335/3 ; 395/3 ; 426/3 ; 484/2 ; 505/3 ; 58:	A;Introns: 56/3 ; 96/1 ; 171/3 ; 199/3 ; 245/2 ; 293/2 ; 335/3 ; 395/3 ; 426/3 ; 484/2 ; 505/3 ; 58:									
Query Match	Query Match									
Best Local Similarity 8.5%	Score 389 ; DB 2 ; Length 860 ;									
Matches 139 ; Conservative 63 ; Mismatches 222 ; Indels 138 ; Gaps 28 ;	Matches 139 ; Conservative 63 ; Mismatches 222 ; Indels 138 ; Gaps 28 ;									
Qy	177 GAHLRKKSQASCQGPQMCNVKAPLGLGSPPRRAKTFASLRSRF-----219									
Db	77 GHVHVKRSIESIDHE-CQFDA---NEDPYPDREAFAMKSMLIRMYKDIRRAEPRHRRDI 132									
Qy	220 --VETLVYADDKR----AAFHGAGLKYRLLTWMAAAK----AFKHPSTIRNPVSLVYTRL 269									
Db	133 LTVBLAYFADDAMWDHFKMKGAAENMHTFIMAVNNIDVLYTQLQPRNIKIVY 192									
Qy	270 VIL-----GSGEEGQPVQGPSSAQAOTLSPCAWQRQGNTPEPSPDHFDTAILFT 317									
Db	193 EILKNIPHLNMKRNHSNCD-----VDRLLDIAFCYQONEINPNPDAPIWMDHALJFS 244									
Qy	318 RDL-----CCVSTCDTQLGADVGTVCDPAPSCALVEDGIGOSAFTPAAHELGHVFMILHNSK 375									
Db	245 GYDLHRNGVKT---VAGYAPVKGMCSGVRSCNTINEGLDFGSVTVTHMGSLSGMHDGN 302									
Qy	376 PCISLNGPLSTSRRHVMAPVMAHVDPPEPWSPCSARFITDQLGQTCARLWVQHNGPQVHNLH-----CILDFLNGYGH-----CLLD 426									
Db	350 -ASANBORMVAKPESBPGQQLTDEQIFPGEWKRHELDQGQTMONICQWVCG-----N 405									
Qy	478 GHAMCQTKHSPWADGTPCGPAQACMGGRCLAMDQLQDFNIPQAGGWPGW---PWGDCSRT 535									
Db	406 GEGSVIRAH-PALEGYTCGEGMICRQGCVQGSCQLRQVTV---GGNSTWDRP---APT 457									
Qy	536 CGG-----GVOFSSRQDCTRPVPRNGKCYERRTRRERSCNTEDCQPGNSALTR 584									
Db	458 CGGRCSQCEIRQIRINMSIROCNPNSSNNGAPCQDDEARGMVCHRDVCNGDSIENYAT 517									
Qy	585 BQCAAYNHRDLFKSPFGPMDFWPRVYGV---PODQCKLTC-----QARALGYYVYLB 635									
Db	518 RVCSRDLDE---NAIPTN-----JUSGEQMOFEQAMCKWILISGSTNIRTVSNF--- 564									
Qy	636 PRVVDGTPCSPDSSVQVQGR 657									
Db	565 ---PDGAPCPGP---GQXCIKGEC 581									
RESULT 10										
T00260	hypothetical protein KIAA0605 - human									
C;Species: Homo sapiens (man)	C;Species: Homo sapiens (man)									
C;Date: 01-Feb-1999	C;Date: 01-Feb-1999									
C;Accession: T00260	C;Accession: T00260									
R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Nomura, N.; Ohara, O.	R;Nagase, T.; Ishikawa, K.; Miyajima, N.; Nomura, N.; Ohara, O.									
A;Title: Prediction of the coding sequences of unidentified human genes										

C:Genetics:
A:Note: KIAA0605
F:46-106/Domain: thrombospondin type 1 repeat homology <THRL>

Query Match Score 8.0%; Score 365; DB 2; Length 951;
Best Local Similarity 33.1%; Pred. No. 7.4e-13;
Matches 104; Conservative 32; Mismatches 132; Indels 46; Gaps 16;

Qy 523 WGPGPWGCGSRTGGGIVFSSSDC---TRPVPRNGKCYGRGTRPRFCNTEDPTGS 578

Db 50 WGEWTWKWTFASRSRGGGTTSQRHCLQRKRSVPGNTRCTGSKYQLCRVQECPP-D 108

Qy 579 ALTFREEQQAA---YHNRDOLFLKSFPQPMWDVPRYTGAVPD-----OCKLTQAR 626

Db 109 GRSPREEQCVFSNSHVNTRH-----QWKPLI---PDDPVHISKSPCDLHC-TT 154

Qy 627 ALGYYYVLEPRVVDGTPCS-PDSSSVCYQGRCTHAGCDRIGS5KKPDKCMVGGDGSGC 685

Db 155 VDGQRQLMVP-ARDGTSCLTLDLQGVCSGKCBPQGQVLFSTHTLQKGICQGDGSSC 213

Qy 686 SKQSSSFRAK---FRIGYNNNTVTPAGATHILVRQGNPGRHSRSTIAKLPDGSYALNGET 743

Db 214 THVTGNYRGRGNAHGLYSLWTHIPIGARDQIVERKKSAD---VIALADAEQGYFFENGRYK 270

Qy 744 LMPSPTDVYLPGAVSLRYSGATASSET---LSSHGPGLAQPFLQLVLI-VAGNPQDTLRY 798

Db 271 -VDSPKNFIAGTV-VKRRPMPDVYTFGTLEYIYAGQPPTNQGIAWVNNQNGKSPSITFEY 328

Qy 799 SFFYPRPTPSTPRP 812

Db 329 TLLQP-PHESRPQP 341

RESULT 11
S60257

meltrin alpha - mouse
C:Species: Mus musculus (house mouse)

C:Accession: S60257
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

R:Yagami-I ironoaba, T.; Sato, T.; Kuriaki, T.; Nabetohima, Y. I.; Fujisawa-set

Nature; 377, 652-656, 1995
A:Title: A metallocoprotease-disintegrin participating in myoblast fusion.

A:Reference number: S60257; MUID: 96026308; PMID: 7566181

A:Status: Preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-303 <YAG>

A:Cross-references: UNIPROT:Q611824; EMBL:D50411; NID:91054586; PIDN:BAA00912.1; PIDN:9105

C:Superfamily: mouse meltrin alpha; disintegrin homology
F:421-503/Domain: disintegrin homology <DIS>
F:349/Active site: Glu #status predicted

Query Match Score 6.8%; Score 313; DB 2; Length 903;
Best Local Similarity 22.7%; Pred. No. 2.4e-13;
Matches 214; Conservative 103; Mismatches 393; Indels 234; Gaps 47;

Qy 38 LLLIASLPLSPARLASPLPREEEIVPEKINGSVL----PGSSAPAR----LLCRHQ 86

Db 15 LLLALAGALLAFLPRAARGMSLWDQRAYEVAVARASLLSKDGPQGSIAPADHPDVLTQHQ 74

Qy 87 AFGETLLELEQDSGIVQVEGLT-VQYL---GQAPELIGGAERGTYLTGTGNDPESVSLH 143

Db 75 LESRDLTSLERNEGLIANGFETHTYLQDGTDVSLTRNHDHCYTHGTHQDAAASVVSLS 134

Qy 144 WDGALLGIGVQYRGAEILHQPLEGGTPNSAGGGAHILRKSPASQGQPMCNVKAFLGSP 203

Db 135 -TCSDLRGLIMENKNTYSLEPKNTDSYKLVPAESMTIQGLCSQHNSNLNTMBDVS 193

Qy 204 SPPRRAKRF---ASLRFVETLVAADDKNAAFHGANL---KRYLLTMMAAAAKAFKHP 256

Db 194 GTSQMARRHXRKRETLYKTVELVIAADNREFQRQSKDLEYKORLIEIANHVDKFYR-- 251

Db 257 SIRNPVSLVTRVLIG---SGEEGQVGPSAAQTLRSFCAWQRGLNTPEDSDPDHFDT 312

Qy 252 ---PANI---RIVVGVWVNDKRCISISQDPFTTRLHFEDWKRKLLPRKS---HDN 300

Db 252 ---PANI---RIVVGVWVNDKRCISISQDPFTTRLHFEDWKRKLLPRKS---HDN 300

Qy 313 ALFPFDQLCCVSTCDTLMGADVGTVCDPARSCAV--EDDGLOSSAFTAAHELGHVFNM 369

Db 301 AQLISGVYFQGT---TIGNAPINSMCTAEQSGGVMHDSDSPUGAVTLLAHELGHNGFM 356

Qy 370 LDHNSRPCISLNGPLTSRHEWMPAHVDPPEPNSPCSARFIDTFLDNGYGHCLDKP 429

Db 357 NDHTLERGCSRCMAAEKGCGC1MNPSTGFPPP-MVFS SCRSRKDLASLEKGMGMCLFLNLPE 415

Qy 430 APLHIFPVTPFGK-----DYYDAHQC-----QLTPGDS-----RHC 460

Db 416 ---VKAOFGGRKCGNGYVEEGEBCDGEPEEECTNRCNATTCLKPDAVCAHGGCEDC 471

Db 461 POLPPPCAALWCGSHINGHNGAMCQ---TKHSP---WAGTPC-GPAQACMGRC-LHM 509

Qy 472 -QLKPEGTA---CRGSNSCDLPEFCITGATAPCPANVYLHGPQCOVDGCGYCYNGQOTHE 528

Db 510 DQLDQNTNIPQAGGWGPWGPGDCSRTICGGYQFSSRSDCTRVPVRNGKY-C-EGRTRP 566

Db 529 QCCTVL-----WGP-----GKPAKAPICFERNVNSACDPYGNCGKDSKSAF 568

Db 567 RSCNTDPCPTGSLATFREEQCAAYNRTDLFKSFPEPPMDWPRYTGAVPDQCKLTQAR 626

Qy 569 AKCELDAKCGK1-----QCOGGASRPVI-----GTNAVSIETNIPQEGGRILCR-- 614

Db 615 -GTHYTLGDDNPDPGLVLAGTKA-EKGICLNRNCQNIS---VFG---VHKCZMQCH 663

Db 616 GDCGCSKQSGSF-----RKFYGYNNVVTIPIGATHI-LVYRQGNPGHHR--SI 725

Qy 664 GRCV-CNNRKNCHEAHWAPPFCDKFGF-----GSTDSGPROADNQGLTGYLV 713

Qy 726 YLALKLPDGSYALNGEYTLM-----PSPTDWWLPGAVSLRYSGATAA 767

Db 714 SILCLLAAGFVYILKRTLMLRLLFTHKCTKTMELRCHVPSRT-----PSGPHLQQAHTTPG 769

Qy 768 SETLISGROPL-----AQPLTIVQVLAGNPDTTRLYSFFTP-----803

Db 770 KGLLMNTRAPHNTFPKDHSILKQNMMDISRLPDLARAYPQLOSPQRVNLPLHQTPRASSGPA 829

Qy 804 RPTPSTP-----RPTPODWLHRAQTLBLRPP 832

Db 830 RPLPASPAVRQAGIRKSPPPQRPLPADPLSRTSLRSTSLVNLTP 873

RESULT 12
T15976 hypothetical protein F08C6_1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Accession: T15976 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

R:Bentley, D. submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid F08C6.

A:Reference number: Z18440

A:Accession: T15976 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-957 <BEN>

A:Cross-references: UNIPROT:Q19204; EMBL:U29378; PIDN:9868185; PIDN:AAA68721

C:Genetics:
A:Gene: CESP:F08C6_1

A:Experimental source: strain Bristol N2

Qy 144 WDGALLGIGVQYRGAEILHQPLEGGTPNSAGGGAHILRKSPASQGQPMCNVKAFLGSP 203

Db 135 -TCSDLRGLIMENKNTDSYKLVPAESMTIQGLCSQHNSNLNTMBDVS 193

Qy 204 SPPRRAKRF---ASLRFVETLVAADDKNAAFHGANL---KRYLLTMMAAAAKAFKHP 256

Db 194 GTSQMARRHXRKRETLYKTVELVIAADNREFQRQSKDLEYKORLIEIANHVDKFYR-- 251

Db 257 SIRNPVSLVTRVLIG---SGEEGQVGPSAAQTLRSFCAWQRGLNTPEDSDPDHFDT 312

Qy 252 ---PANI---RIVVGVWVNDKRCISISQDPFTTRLHFEDWKRKLLPRKS---HDN 300

91	ERKGGSGLDFGSTDS	--CHYHGYKEKYAAISNCDG	--RIVSESNRKQG	135	Query Match Score 5.9%; Best Local Similarity 23.1%; Pred. No. 1.6e-0; Mismatches 97; Conservative Matches 161; Index 175; Gaps 38;
125	GTVLTTINGDPESVASHWDGALLGVLYQYGAELHQLPLEGTPNAGPAAHILRK	184	Db	5 LLVTCILAAAPPYQSSSIILESGNVYDEVYTPRKY--TALPKGAVQPKYEDAMQFLKVN	62
136	--KGTVDGPI-----TIVHPPDFHAAHRSRATEN---	173	Qy	37 LLLILIASLIP-----SARLASPLPREEVEPEKLINGSVLP-GSAPA--RLLCRLQAF	88
185	SPASQGQPMCNVAKPLGSPSPRRAKRFAASLRSRFVETLVVADDIKMAAF-	233	Db	5 LLVTCILAAAPPYQSSSIILESGNVYDEVYTPRKY--GQAPELLGGAEPEGTLYLTGTINGDPESVASHWD	145
174	ETLAGE-----PRDFCLDNVVTBESLVEDESAFAEDVPTVGTQBLT	214	Qy	89 GETLLELBDGSVYOVEGLTVQYL--GQAPELLGGAEPEGTLYLTGTINGDPESVASHWD	145
234	-----HGA-----GLKRYLITVAAAFAKHPSPSRNPVSLV	265	Db	63 GEPVVLHLGRNKGLFLSKDYSETHYSPDGREITTYPLVEDCYHGRENDSTASISAC	122
215	QQSDLIVEFLAVFTDENLWRHFSSKXHGGMADRKQDQYTLTLNNIQIMYQOPTASPLTFR	274	Qy	146 GGALLGVLYQYGAELHQLPLEGGTPNASSGPGAHILRKPSASQG--PMCNVKAPLGS	202
266	VTRVLVIGSGEEGPQVG-----PSAAQTLRSFCAWQRLGNTTPDDPDHFDTAILFTRQD	320	Db	123 NG-LKGHPFLQLOGENYLIPLK--LPDSE--AVAWKYENVEKEDALEKMGVTQNWES	175
275	VARYEVLTROPSALAGLYLHNHNGRAQMFLDPECTYQRNLAVR-----WDHAIMLTCYD	327	Qy	203 PSPRBRACKFASL-----REFEVTLVYADDKMAAFIGAGL--KRYLITVMAAAAKA	252
321	L-CGVGSTCDTLGRNADGTVCDPAPRSACLAIVEDDGQSOAFTAHELGHVNMLHDNSKPCJ-	378	Db	176 YEPITKASQSLVTTAHEQKYNPFRFVBLFLVVDKAMVTKONGDLDCKTRMYBVNTVNEI	235
328	IHRGAGSRSISIGTARLDGMDPWNCTLAEGJLDTSAFTHGLHRPTELKDHKSDTL	387	Qy	253 FKHPSIRNPVSLVYTRVLVSGEGPGQVCPQVPSAAOTLRSFCAWQRLGNTTPDDPDHFDT	312
379	-SLNGPIS-----TSRHHMAPTMWHP-----BEPMS-----	405	Db	287 AQLTAIDDRV----IGLAYVGSMCHPKRSTGIIQDYSBENLVLVAVIAHEMGENLGI	341
388	TGTFCGPSPSKWCQLGRCVPTWGTNBQIPTVQHVAAPVVTILPSRSDGSNGWGATICSQTC	447	Qy	236 YRMYIH--VALVYGE--IWSNEDKITYKPEAGTYLNAGEWRK--TDLILTRKCH-DN	286
406	-----PCSAFPIITDFLDNGYGHCLDKPRAPIHLPLVTPGKDYDADROC--	449	Db	313 AILFTRQDLICGVSTCDTLGRNADGTVCDPAPRSACLAIVEDDGQSOAFTAHELGHVNMLHDNSKPCJ	369
448	NGLGSVGLAARRTCSAPYPA-----NGCSDCTGSTSRAVL-----CSRQGR	491	Qy	370 LDHNSKPCISLNGPLSTSRRH--VMAPVMAHVDPPEWSPGCSARFITYDLEONGYGHCLDK	427
450	-----QLTGPDPDSRHCPQLPPCPAALWCSGHINGHAMCQTKH	486	Db	342 NHD-----SGYCSGDIYACIMRPEIS--PEPSTFNSCSYFECDFMHNHNPECLNE	392
492	ASKVDEYISDKCMEQKRLKNDRFL-EKGSQ--LNRPTFQRAKVFCD--VOQHGXGQNY	547	Qy	428 PEAPLHLPPVTFP-----GKDYD--ADRCQCOLTFGDDSRHCPQLPPCPAALWCSGHINGHAMCQTKH	472
487	SPVA-----DGTGPDPGAQCTMGRCILHM-----QLOQDNIP-----QAGGW	523	Db	393 -----PLGTDIISPPVCGNELLVEGECDCGTPPENCO-----NEC----CDAATCKLK	436
548	RPGDNLPDGTSGCSDGYCDYCLGBCLNACNNNALISRDQSCPDTTCPITDQSSSVYRGQW	607	Qy	473 SGHLNQHANC--QTKHSP----WADGTPCPGAOACMGGRCLHNMQLQDFNIPQAGGWGP	525
524	GPWGPWGDSCSRTCGGGVQFSRDRCTRPTVPRNGKTYCERTRPNSCTEDCPT-----	576	Db	437 SGSOQGHGDCBQCKPSKSCTECRASMSBDAEHCTG-----	474
608	GTWSLWTSCTATGGYKRNACST-----GQCBENDETEBVCSSBSCPVLVNE	661	Qy	526 WGPWGDSCSRTCGGGVQFSSSRDCTRPTVPRNGKTYCERTRPNSCTEDCPT-----	576
577	-----GSALTPREEQCAAYNHRDLDLKPSGPMDWPRYTVGAPODQCKLT	622	Db	475 -----QSSECPADVFHKNGQPC--LDTNGYCNQNCPTIMYHQCYDLF	514
662	WSTWTWNHCVSVCGRGSQARYRKCLS--PHRTLAF-DCPG-----ENRVT	704	Qy	577 GSALTPREEQCAAYNHRDLDLKPSGPMDWPRYTVGAPODQCKLT	629
623	CQAR-----ALGTYVV-----	650	Db	515 GADTYEAEDSCFERNQKGNY-----GXCRKENGKNCAPEDVTKGRYLYCKDMSNPGQ	567
705	NEIRITPFKARSYIMCSTRNKIKRNTISEKNTIEVRSCDNDGPNAIGWTGWTGGWSTST	764	Qy	630 -----YYVYLPFR----VYDGTGPSCPDSSSVQVGRCI	658
651	VCVQG-----RCHAGCDRTGSKKKEDKCMY--CGGDG-----SGCSKOSG	690	Db	568 NNPKCMFYSNEDEHKGMVLFPGTKCA--DGKVCNSNGHCV	603

RESULT 13
 G02390
 disintegrin-like metalloproteinase MDC15 (EC 3.4.24.-) - human
 55270
 catrocollastatin precursor - western diamondback rattlesnake
 C;Species: *Crotalus atrox* (western diamondback rattlesnake)
 C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
 C;Accession: 55270
 R;Zhou, Q.; Smith, J. B.; Grossman, M. H.
 R;Biochem. J. 307, 411-417, 1995
 A;Title: Molecular cloning and expression of catrocollastatin, a snake-venom protein from western diamondback rattlesnake
 A;Reference number: 55264; MUID: 9521603; PMID: 7731877
 A;Accession: 55270
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-609 <R>
 A;Cross-references: UNIPROT:Q90282; GB:U21003; NID:9710353; PIDN: AAC59672.1; PID: 9710354
 C;Superfamily: mouse melinin alpha; disintegrin homology

A; Molecule type: mRNA
 A; Residues: 1-461 <MCR>
 A; Experimental source: articular chondrocyte
 C; Comment: This protein is a membrane bound protein and involved in cell/cell and cell/matrix interaction
 C; Superfamily: mouse meltrin alpha; disintegrin homology
 C; Keywords: hydrolase; metalloprotease; zinc
 P; 148-352/503/Domain: disintegrin homology #DIS
 P; 338/503/Domain: zinc (Hie) #status predicted
 P; 349/Active site: Glu #status predicted

Query Match Score 268.5; DB 2; Length 814;
 Best Local Similarity 24.3%; Pred. No. 2.2e-10;
 Matches 187; Conservative 82; Mismatches 259; Gaps 45;

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  QY 34 LYMLLILIA-SULPSARLSPR-----EEEIVPEKLNGSVPG-----74
  Db 5 LLWALGLLQAGSPPS---WPLDNIGTTEQQAESEKAAPRPLEPOVQLDQLPISUKY 60
  QY 75 -SGAPARLICRQLQAFGETLILIEQD-----SGVQV-EIGHTVQYIQA 115
  Db 61 LQTSLPEPRKIELDGDSHILELQNBLVPERPTLVYQDGTIVSSEGTILENCYQ 120
  QY 116 PELLGGAEETGY-----LTGTINGDPEVSVASLHNDDGALLG-VLQXRGAELHLOPL 166
  Db 121 GVRGYA-GSWSVICTCGSLRGLVVLPERSTLEQPGDQGPPQTISRIDLHLP-- 175
  QY 167 GGTPNSAGGFGAAHLLRKPSAGGSPGPMTCVKAPLGSPPRPRAKRPAASLSEFELVVA 226
  Db 176 -----GHTCAWSRVEHTQTTP---EHPHQGRIRRRL--DVTETKTVLIVVA 221
  QY 227 DDKWAAFHGAGLKRKYLITVAAAAKAFKPSIRN-PVSLVV-----TRVLIG--- 273
  Db 222 DHSEA-----QKY-----RDFQFLINNKTELEVALLDFFPRFLNRYALVGEAW 265
  QY 274 SGEFPQVQPSAAQTLRSFCAWORGLNTEPDSDPHFTDAILFTRODLQGVSTCDLGMA 333
  Db 266 TQDRLVEISNPATVLEFLHWRDAAHLRLRP---HSDAQLVGTSGG---PTVGM 317
  QY 334 DVGTVCDPDRSCAIYEDDG--LQSAFTAHHELGHVNMHLD--NSKPCISLNGPLSTS 387
  Db 318 IONSIICSPDFFGGVNMHDHSATLTSILGVAASSAHELGHSLGDHDLPGNSCPC---PGPAPAK 374
  QY 388 RHVMAFPVMAHID--DPEPNSPCASRIFTDLDNGYGHCLDK_PEAFLHLPV_TFPGKDY 443
  Db 375 TCIME---ASTDPEFLQLNFSRCALEYKALLDGNGSCFERLPSL--PMIAFCGIMF 428
  QY 444 -DADRCQLTFGPDSRHCPOLPPCAALWGSNHNGHAM-----COTKHSFW--- 489
  Db 429 VEPGQCDGPFLDD---C-VDPPCCDSLTCOLRPGQAQCSADGPCCQNCQLRPSWQCRFT 483
  QY 490 -----ADGTPCPAQA-CMGRCL_HMDQDODNTFQAGGGW 524
  Db 484 RGDCDLPFECPCPDSSQOPDVSLGDBPAGQAVCMHGRCASTAQQCCSL--- 534
  QY 525 PWGPWGDCSRSRIGCGGQFQSSRDCTRPVPRNGKYGCEGRTRFRSCNTEDCPTGS---ALTF 582
  Db 535 -WGP-----GAQAPAPICLQQTANTRG-----NAFGSGCRN--PSGSXVSCP 573
  Db 583 REBQCAAYNHRTDFFKSPGP-----DMDPRTYTGVAPODOCKLTCAA 625
  QY 574 RDAICGQLQCCQGRTQPLGTSRDLWEITDVGTELNCMSVHLDLG---SD----- 622
  QY 626 RALGYYTTLPEPRV-VDGTSPCPSDSSVYQSRCRIHAGCDRLIGSKKKKFDK 675
  Db 623 -----VAQPLTLPGTACGP--GLVCIIDRCQRYD--LIGAQECRSSRC 661
  
```

R; Nishida, S.; Fujita, T.; Kohno, N.; Atoda, H.; Morita, T.; Takeya, H.; Kido, I.; Paine, R; Nishida, S.; Fujita, T.; Kohno, N.; Atoda, H.; Morita, T.; Takeya, H.; Kido, I.; Paine, Biochemistry 34, 1771-1778, 1995
 A; Title: cDNA cloning and deduced amino acid sequence of prothrombin activator (ecarin) 1
 C; Comment: This protein is a membrane bound protein and involved in cell/cell and cell/matrix interaction
 A; Reference number: A55796; MUID:95151760; PMID:7849037
 A; Accession: A55796
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-616 <NIS>
 A; Cross-references: UNIPROT:Q90495; GB:D32212; NID:9717090; PID:BA006910.1; PID:9717091
 C; Species: Echis carinatus (saw scaled viper)
 C; Date: 05-Jan-1996 #Sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
 C; Accession: A55796

Search completed: April 1, 2005, 12:52:34
 Job time : 55 secs

RESULT 15
 A55796
 ecarin precursor - saw-scaled viper
 C; Species: Echis carinatus (saw scaled viper)
 C; Date: 05-Jan-1996 #Sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
 C; Accession: A55796

DR	GO:0007229; P: integrin-mediated signaling pathway; IEA.	721	GHRSTYLAALKLPDGSYAALNEYTILMPSPTDVLPGAVSLRYSGATASETLSGHGPALQP	780
DR	GO:0006509; P: proteolysis and peptidolysis; IEA.	721	LTLQVLYVAGNPDTTRYSFFVRPTPSTPRTPQDNLHRRQILELRRPWAQK	837
DR	InterPro; IPR006546; ADAM cysteine.	781	LTLQVLYVAGNPDTTRYSFFVRPTPSTPRTPQDNLHRRQILELRRPWAQK	837
DR	InterPro; IPR010294; ADAM spacer1.	781	LTLQVLYVAGNPDTTRYSFFVRPTPSTPRTPQDNLHRRQILELRRPWAQK	837
DR	InterPro; IPR001590; Peptidase_M12B.			
DR	InterPro; IPR006035; Pept_M_Zn_BS.			
DR	InterPro; IPR000884; TSP1.			
DR	InterPro; IPR000895; TSP1.			
DR	PFAM; PF05986; ADAM_spacer1; 1.			
DR	PFAM; PF01421; Reprolysin; 1.			
DR	PRINTS; PR01705; TSP1; 1.			
DR	SMART; SM00249; TSP1; 1.			
DR	PROSITE; PS50215; ADAM_MEPRO; 1.			
DR	PROSITE; PS50092; TSP1; 1.			
DR	PROSITE; PS00142; ZINC_Protease; UNKNOWN_1.			
KW	Integrin.	837 AA:	90149 MW:	3B91C51E54EFC5F CRC64;
SEQUENCE				
Query	Match 99.3%; Score 4538; DB 2; Length 837;			
Best Local Similarity 99.3%;	Pred. No. 5.4e-284;			
Matches 831; Conservative 3; Mismatches 3; Indels 0; Gaps 0;				
Db	1 MSQGQSHPGRGLAGRWLWGAQPCUCLPVLPTPLSMVWLLILLASLPSARLASPLPREE 60			
Db	1 MSQGQSHPGRGLAGRWLWGAQPCUCLPVLPTPLSMVWLLILLASLPSARLASPLPREE 60			
Qy	1 IVFPEKLNGSVLPSSGAPARLCLQAFGETLLEQDSGVQEVEGTVYQIYGQAPELIG 120			
Qy	1 IVFPEKLNGSVLPSSGAPARLCLQAFGETLLEQDSGVQEVEGTVYQIYGQAPELIG 120			
Db	1 IVFPEKLNGSVLPSSGAPARLCLQAFGETLLEQDSGVQEVEGTVYQIYGQAPELIG 120			
Qy	121 GAEPGTLYLITGNGDEPESVSLGGALLGVLQYRGAHLQPLEGGTPNSAGGGPAH 180			
Db	121 GAEPGTLYLITGNGDEPESVSLGGALLGVLQYRGAHLQPLEGGTPNSAGGGPAH 180			
Qy	181 LRRKSPASGGPQPMCNVKAPLGSPSPRPRAKRFLSRSRVEVTLVADDMAPHAHGAIKR 240			
Db	181 LRRKSPASGGPQPMCNVKAPLGSPSPRPRAKRFLSRSRVEVTLVADDMAPHAHGAIKR 240			
Qy	241 YLTVMAAAATAKPHISIRNPVSLVYTRVLIGSGEEGPGVQGPSSAQTLSFCWQRGIN 300			
Qy	241 YLTVMAAAATAKPHISIRNPVSLVYTRVLIGSGEEGPGVQGPSSAQTLSFCWQRGIN 300			
Db	301 TPESDDDHFDTAILTRDQCGSTCDTGMADIGTVCDPARSCTAVDDGLOSATAA 360			
Qy	301 TPESDDDHFDTAILTRDQCGSTCDTGMADIGTVCDPARSCTAVDDGLOSATAA 360			
Db	301 TPENSDHFDTAILTRDQCGSTCDTGMADIGTVCDPARSCTAVDDGLOSATAA 360			
Qy	361 HBLGHVNMLDNNSKPC1SNGPLSTSRYMAPMAHDPDEEPNSPCARFITDLDNY 420			
Db	361 HBLGHVNMLDNNSKPC1SNGPLSTSRYMAPMAHDPDEEPNSPCARFITDLDNY 420			
Qy	421 GHCLDKEPAHLPLTTFGKDYDAQRQCOLTFGPDSRHCQPLPPCAALWCSGHLNHA 480			
Db	421 GHRLDKEPAHLPLTTFGKDYDAQRQCOLTFGPDSRHCQPLPPCAALWCSGHLNHA 480			
Qy	481 MCOTKHSPEWADGTPCGPAQACMGCRCLHMDQDFNTPQAGGWGPMGNGDSCSRTCGGGV 540			
Db	481 MCOTKHSPEWADGTPCGPAQACMGCRCLHMDQDFNTPQAGGWGPMGNGDSCSRTCGGGV 540			
Qy	541 QPSRSDCTRPVPRNGGKXCEGRTRPSCNTEDCPGTSALTFREREQCAATNHRDLFKSF 600			
Db	541 QPSRSDCTRPVPRNGGKXCEGRTRPSCNTEDCPGTSALTFREREQCAATNHRDLFKSF 600			
Qy	601 PGMDWVPRYGAPODQCKLTCQARALGYTYLEPRVNGDTPCSPDSSVCYQCRCIHA 660			
Db	601 PGMDWVPRYGAPODQCKLTCQARALGYTYLEPRVNGDTPCSPDSSVCYQCRCIHA 660			
Qy	661 GCDRIIGSKKKFDKCMVGGSGCSKGSFRKRYGVNNVTTIPAGATHILYQCGNP 720			
Db	661 GCDRIIGSKKKFDKCMVGGSGCSKGSFRKRYGVNNVTTIPAGATHILYQCGNP 720			
Qy	721 GHRSTYLAALKLPDGSYAALNEYTILMPSPTDVLPGAVSLRYSGATASETLSGHGPALQP			

Db	359	AAHLGHIVFSMLHDNSKQQTGLNGPESIQRHVMAPVMAHVDPEEPWSPSARFIDFLDN	418	RL	Nature 420:563-573 (2002).
QY	419	GYGHCLLDPEAPHLHPTFPGKDYDAHQOCQLTFGPDRHCPOLPPCAALWCSGHING	478	[4]	SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=whole body; MEDLINE=2049374; Published=11.04.2159; DOI=10.1101/gr.145100;
Db	419	GFHCLLDPEAPHLHPTFPGKDYDAHQOCQLTFGPDRHCPOLPPCAALWCSGHING	478	RC	RC Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; RA "Normalization and selection of cap-trapper-selected cDNAs to RT prepare full-length cDNA libraries for rapid discovery of new genes"; RA Genome Res. 10:1617-1630 (2000).
QY	479	HACQTKRHSKPSWADCTPCGAQACMGRCHMDQDQFNTPQAGGWGPGWGDCSRCTCG	538	RL	[5]
Db	479	HACQTKRHSKPSWADCTPCGAQACMGRCHMDQDQFNTPQAGGWGPGWGDCSRCTCG	538	RN	SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=whole body; MEDLINE=20530913; Published=11.07.6861; DOI=10.1101/gr.152600;
QY	519	GVQFSSRDTTRPVRNGGKCYGERTRFRSCNTEDCPTPSALTFREEQAAINHRTDLFK	598	RC	RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P., RA Konno H., Akiyama J., Nishi K., Kitisunai T., Teshiro H., Itoh M., RA Sumi N., Ishii Y., Nakamura M., Nishime T., Harada A., RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., RA Fujiwaka S., Inoue K., Togawa Y., Iizawa M., Ohara E., Watahiki M., RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RA "RIKEN integrated sequence analysis (RISA) system-394-format RT sequencing pipeline with 384 multicapillary sequencer.," RA Genome Res. 10:1757-1771 (2000).
Db	519	GVQFSSRDTTRPVRNGGKCYGERTRFRSCNTEDCPTPSALTFREEQAAINHRTDLFK	598	RN	[6]
QY	599	SFPPCPMDWPPRTGVAPOQOQLCTQAZBALGTYVLEPRVVDCTPCSDSSSVICRCI	658	RP	SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=whole body;
Db	599	NFPCPMDWPPRTGVAPOQOQLCTQAZBALGTYVLEPRVVDCTPCSDSSSVICRCI	658	RC	RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., RA Fukuda S., Furuno M., Hanasaki T., Hara A., Hashizume W., RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S., RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., RA Seito R., Seiichi H., Sakai C., Sakai K., Sakazume N., Sano H., RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., RA Tagawa A., Takahashi F., Takaku-Akaihira S., Takeda Y., Tanaka T., RA Tomaru A., Toy T., Yasumori A., Muramatsu M., Hayashizaki Y.; RA Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
QY	779	QPTTLQVLAGNPDTLRLRYSFFT-PRPTPSPTRPTQDWLRLRQLLETLRRLRPPVAGR	836	DR	DR EMBL: AK083334; BAC38944.1; -.
Db	779	BPPTLQVLAGNPONARLRYSPFVPRPVPSPTRPTQDWLRLRKSQILELRRRSLWAGR	838	DR	DR HSSP; P07996; 1LSL.
QY	837	K 837	DR	DR MEROPS; M12.22/1; -.	
Db	839	K 839	DR	DR MCD; MGI:1339949; Adamt84.	
QY	837	K 837	DR	DR GO; GO:00422; P: metalloendopeptidase activity; IEA.	
Db	839	K 839	DR	DR GO; GO:0006508; P: proteolysis and peptidolysis; IEA.	
RESULT 5					
ID	QBBNJ2	PRELIMINARY;	PRT;	845 AA.	
AC	QBBNJ2	(TREMBLrel. 23, Created)			
DT	01-MAR-2003	(TREMBLrel. 23, Last sequence update)			
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)			
DE	Mus musculus	9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D03041M02 product: a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4, full insert sequence.			
DE	Mus musculus (Mouse)	Name=Adamt8;			
GN	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.			
OS	OC	OX NCBI_TaxID=10090;			
QY	1	SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=whole body; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;	RP	RP SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=whole body; RT "Punctual annotation of a full-length mouse cDNA collection."; RT "High-efficiency full-length cDNA cloning.";	
QY	2	RA RIKEN_PANTOM Consortium; RA "Functional annotation of a full-length mouse cDNA collection.";	RP	RP SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=whole body; RT "Punctual annotation of a full-length mouse transcriptome based on functional annotation of the mouse transcriptome.";	
QY	3	RA Nature 40:685-690 (2001).	RP	RP SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=whole body;	
QY	4	RA The RIKEN Genome Exploration Research Group Phase I & II Team;	RC	RC The RIKEN Genome Exploration Consortium,	
QY	5	RA "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";	RC	RC "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";	
Db	61	1 YPPPEKLE-SVLPGSGAPARLICRLQAFGETLLELRLQDSCVQEGLTVQYLGQAPELL 119	DB	1 MSQTGSHPGRGLAQRWLGQAPCLLPIVPLSMWVWLLLPLSLPSARLASPLPREE 60	
Db	68	6 YPPPEKLE-SVLPGSGAPARLICRLQAFGETLLELRLQDSCVQEGLTVQYLGQAPELL 127	DB	13 MSQNLGLHPRGLTGHMLRQFQPPL---PLHTRQWRLLLAFLSLWAPSPLPREE 67	

Qy	120	GGAPGTYLGTGTINGDPEVASLHWGGCAALGVLORYGAELHLQPLEGGTPNSAGGPGAH	179	RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S. S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Halton B., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimes J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnurch A., Schein J.E., Jones S.J., Marrs M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Qy	128	GGAPGTYLGTGTINGDPEVASLHWGGCAALGVLORYGAELHLQPLEGGTPNSAGGPGAH	187	RA RA
Db	180	ILRKSPASQGPMCNYKAPLGSPPSPRRAKRFAASLRSRVEYLVYADDKMIAAFHGAGIK	239	RA RA
Qy	188	ILRKSPASQGPMCNYKAPLGSPPSPRRAKRFAASLRSRVEYLVYADDKMIAAFHGAGIK	247	RA RA
Db	240	RYLTVMMAAAKAKFHKPSIRNPVSLVTRVLIGSGEGBQGPSSAAQTLRSFCAWQRLG	299	RA RA
Qy	248	RYLTVMMAAAKAKFHKPSIRNPVSLVTRVLIGSGCGBQGPSSAAQTLRSFCAWQRLG	307	RA RA
Db	300	NTPEPDSPDHFDTAILFTRDLCGVSTCDLGMADYGTVDPARSCIVEDGLOSAFTA	359	RT RT
Qy	308	NTPEPDSPDHFDTAILFTRDLCGVSTCDLGMADYGTVDPARSCIAVEDGLOSAFTA	367	RT RT
Db	360	AHELGHVFMLHDNSKPC1SLNGLPLSTSRRHMAAPVMAHVDPEEPWSPSARPITDLDNG	419	RL RL
Qy	368	AHELGHVFMLHDNSKPC1SLNGLPLSTSRRHMAAPVMAHVDPEEPWSPSARPITDLDNG	427	DR DR
Db	420	YGHCLLDKPEAPLHLPVTEPGKDYADRCQCLTGFDPDSRHCPOLPPCAALMGSGHNGH	479	DR DR
Qy	428	YGHCLLDKPEAPLHLPVTEPGKDYADRCQCLTGFDPDSRHCPOLPPCAALMGSGHNGH	487	DR DR
Db	480	AMCQTKHSPWADGTPCGPQACMGCRCLMDQDENSFOAAGGWMGPWGDGSRTCFCGG	539	DR DR
Qy	488	AMCQTKHSPWADGTPCGPQACMGCRCLMDQDENSFOAAGGWMGPWGDGSRTCFCGG	547	DR DR
Db	540	VQFSRSDCTRPVPRNGKTYCEGRTRTRFRCNTEDOPTGALTTREEQCMAYNHRDTLIFKS	599	DR DR
Qy	548	VQFSRSDCTRPVPRNGKTYCEGRTRTRFRCNTEDOPTGALTTREEQCMAYNHRDTLIFKS	607	DR DR
Db	600	FPGPMDWPRYTGVAQFDQCKLTICARALGYYYLPEPRVTDGTPCSPDSSVCYQGRCH	659	DR DR
Qy	608	FPGPMDWPRYTGVAQFDQCKLTICARALGYYYLPEPRVTDGTPCSPDSSVCYQGRCH	667	DR DR
Db	660	ACGDRIGSKKEFDKCMVCGDGSCKSKQGSFRKFRYGSVTTIPAGATHILVRQGN	719	DR DR
Qy	668	ACGDRIGSKKEFDKCMVCGDGSCKSKQGSFRKFRYGSVTTIPAGATHILVRQGN	727	DR DR
Db	720	PGHRSITYLALKLPDGSYALNGBYLMPSPDVTVLGAVSLRYGATAASSETLSGHGPLAQ	779	Qy Qy
Qy	728	SEKLSITYLALKLPDGSYALNGBYLMPSPDVTVLGAVSLRYGATAASSETLSGHGPLAQ	787	Db Db
Db	780	PLTLQVLAGNQFDTRLYSFPVPRPTSPTRPTQDWLRRAQLEIIRRPRWAGRK	837	Qy Qy
Qy	788	PLTLQVLAGNQFDTRLYSFPVPRPTSPTRPTQDWLRRAQLEIIRRPRWAGRK	845	Db Db
RESULT 6				
ID	QK384	PRELIMINARY;	PRT;	833 AA.
AC	QK384;	22, (TREMBLrel.	Created)	
DT	01-OCT-2002	22, (TREMBLrel.	Last sequence update)	
DT	01-MAR-2004	26, (TREMBLrel.	Last annotation update)	
DB	Adamt84	4 protein.		
GN	Name=Adamt84;			
OC	Mus musculus (Mouse).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OC	NCBI_TaxID=10090;			
RN	[1]	SEQUENCE FROM N. A.		
RP	SEQUENCE FROM N. A.			
RC	SEQUENCE FROM N. A.			
MDLINE	-22389257	TISSUE=Mammary tumor. C3; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RX	STRASBERG R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heleb F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L.,			
RA	300 NTPESDPDHFDTAILFTRDLCGVSTCDLGMADYGTCDPARESCTAYEDGHQSFTA 359			
RA	306 AHELGIVFNMHDNSKPC1SLNGLPLSTSRRHMAPMAHVDPEPWSPCSARFIDFLDNG			
RA	324 RYLTVMMAAAKAKFHKPSIRNPVSLVTRVLIGSGEGBQGPSSAAQTLRSFCWQRLG			
RA	332 1 MSQNGLHPERGLTGWLRFQPEL---PLRIVQWRLLLAFLSLAWPSPLREE			
RA	350 1 MSQTGSHPGRGLAGRMWGAQPCLLPVLPSWLVWILLIILSLPSARLASPLPREE			
RA	356 1 MSQNGLHPERGLTGWLRFQPEL---PLRIVQWRLLLAFLSLAWPSPLREE			
RA	360 1 MSQTGSHPGRGLAGRMWGAQPCLLPVLPSWLVWILLIILSLPSARLASPLPREE			
RA	374 61 IVPPBKLN-G-SVLPGSGAPARLICRQLQAFGETLILLEQDGSVYQVEGLTIVYLGQAPELL			
RA	382 SEQUENCE 833 AA; 90079 MW; 4CEC83DFBC3AA619 CRC64;			
RA	390 56 IVPPBKLN-G-SVLPGSGAPARLICRQLQAFGETLILLEQDGPMEMLLEQDGPVQVEGLTIVYLGQAPML 115			
RA	408 120 GGAEFTYLTGTINGDPEEVASLHWGGALLGTVQYRGAEHLQPLBEGTPNSAGGPGAH 179			
RA	416 116 GGAEFTYLTGTINGDPEEVASLHWGGALLGTVQYRGAEHLQPLBEGTPNSAGGPGAH 175			
RA	434 180 ILLRKSPASQGPMCNVKAFLPQKSPSPPRKEFKAISLSPFVETLVADKMAAFLHGAGIK 239			
RA	452 176 ILLRKSPASQGPMCNVKAFLPQKSPSPPRKEFKAISLSPFVETLVADKMAAFLHGAGIK 235			
RA	470 240 RYLTVMMAAAKAKFHKPSIRNPVSLVTRVLIGSGEGBQGPSSAAQTLRSFCWQRLG			
RA	488 236 RYLTVMMAAAKAKFHKPSIRNPVSLVTRVLIGSGEGBQGPSSAAQTLRSFCWQRLG			
RA	506 300 NTPESDPDHFDTAILFTRDLCGVSTCDLGMADYGTCDPARESCTAYEDGHQSFTA 359			
RA	524 296 NTPESDPDHFDTAILFTRDLCGVSTCDLGMADYGTCDPARESCTAYEDGHQSFTA 355			

Db	Q1	Q2	Query Match	Match	Score	DB	2;	Length
Db	416 YGHCLLDKPEAPLHLPATFPKDXADRCQLTFPGDSSHCPOLPPCAULMCSGHNLHG	475	Best Local Similarity	85.2%	Score 3894;	DB 2;	Length 893;	
Db	480 AMCOTKHSKPAWDTCPGCAQACMGRCLHMDLQDENTPQAGMGPNCGCSRTCGGG	539	Matches 732;	Conservative 25;	Prod. No. 1..3e-22;			
Db	476 AMCOTKHSKPAWDTCPGCSQACMGRCLHMDLQDENTPQAGMGPNCGCSRTCGGG	535	Missmatches 68;	Indels 18;	Gaps 5;			
Db	540 VQFSSRDCTRPVDRNGGCKCEGRTRPASCTEDCPGSALETFREOCATNHRDIFKS	599	Qy	1 M50TGSHIGRGLAGRMWGAQPCDLPVPLSLVWLLLULASLPLSPARLASPLPREE	60			
Db	536 VQFSSRDCTRPVDRNGGCKCEGRTRPASCTEDCPGSALETFREOCATNHRDIFKS	595	Db	63 M50QMGLPFRRLGTLGHWRFPQPL---	60			
Db	599 PFPMDWVTPRTGVAPODQCKLTCQARALGTYVLEPRVDGTPCSPDSSVVCQGRCH	659	Qy	61 IYVPEKING-SVLPGSGAPARLICRLOAFGETLLELQDGSYQVEGLTVQVIGOAPEL	119			
Db	596 PFPMDWVTPRTGVAPODQCKLTCQARALGTYVLEPRVDGTPCSPDSSVVCQGRCH	655	Db	118 IYVPEKINGSSILPGSGVPARLILYRPAFGEMILLEBQDGPVQVEGTVQYQQAPENL	177			
Db	660 AGCDRIGSKKKEDPKCMVCGGDSGCSRSQSGSPRKFKFYGYYNNVTTAGATHILVROQGN	719	Qy	120 GGAEPGTYLTGTINGDPESVASHWDGALLSGLVQYRGAEHLQPLEGTPNSAGGPQAH	179			
Db	656 AGCDRIGSKKKEDPKCMVCGGDSGCSRSQSGSPRKFKFYGYYNNVTTAGATHILVROQGN	715	Db	178 GGAEPGTYLTGTINGDPESVASHWDGALLSGLVQYRGAEHLQPLEGALNSAGGPQAH	237			
Db	720 PGHRSIVLAKLKDPSYALANGETLMLSPTDVYLPGAVSLRYSGATASETLGHPLAQ	779	Qy	180 IYRKSPASGGPDMCNVKAPLSSPSPRRAKFAISLRFVETLVADDKMAAFHGAGLK	239			
Db	716 SGHLSKIVLAKLKDPSYALANGETLMLSPTDVYLPGAVSLRYSGATASETLGHPLAQ	775	Db	238 IYRKSPASGGPDMCNVKAPLSSPSPRRAKFAISLRFVETLVADDKMAAFHGAGLK	297			
Db	780 PLTQLVLYAGNPDDTRIYSFVPRPPTSPRETPQDWLRHQAQILELIRRWPAGRK	837	Qy	240 YVLLTVMAAAAKAFKHPISRNTPVSLVYTRVLVIGSREEGPVOY---	PSAAQTLRSFCA	294		
Db	776 PLTQLVLYAGNPONARLRSYFFVPRVFSPTPRPPQDWMLQRRAEILKLRKPWAGRK	833	Db	298 YVLLTVMAAAAKAFKHPISRNPNLVTRLVI-GRARKGPKNQVPPPYAASAPGS---	353			
Db	Q6A017 PRELIMINARY; PRT; 893 AA.		Qy	295 WQRGLNTPEDSPDPHDFTAILFTRDQLGVSTCDTLMADGVTRCDPARSCLIVEDDGLQ	354			
Db	Q6A017, 25-OCT-2004 (TREMBLrel. 28, Created)		Db	354 --GASPPLTQIQLTTAILFTRDQLGVSTCDTLMADGVTRCDPARSCLIVEDDGLQ	410			
Db	DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)		Qy	355 SAPTAHELGHVNMLHDNSKCI SINGPLSRSRHNAAPVMAHVDPEPWPSARPTD	414			
Db	DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)		Db	411 SAFTAHELGHVNMLHDNSKCI SINGPLSRSRHNAAPVMAHVDPEPWPSARPTD	470			
Db	DB MKIAA688 Protein (Fragment).		Qy	415 FLDNGYGHCLLDKPEAPLHLPTVFPKDYDADRCQLTFCGPDSSRHCPCOLPPCAALWCSG	474			
Qy	GN Name=mkiaa688;		Db	471 FLDNGYGHCLLDKPEAPLHLPTVFPKDYDADRCQLTFCGPDSSRHCPCOLPPCAALWCSG	530			
Qy	OS Mus musculus (Mouse).		Qy	475 HUNGHAMCQTKHSKPAWADGTPCPGAQACMGGRCHMMQLQDENIPQAGCQWGPNGPQWGDCSR	534			
Qy	OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;		Db	531 HUNGHAMCQTKHSKPAWADGTPCQSSACNGGRCHMMQLQDENIPQAGCQWGPNGPQWGDCSR	590			
Qy	NCBI_TaxID=10090; RN [1]		Qy	535 TCGGGTQESSRDTCTPYRNGSKYCEGRTRPSSCTEDCPGCSALTFREEQCAAYNHT	594			
Qy	RP SEQUENCE FROM N.A.		Db	591 TCGGGTQFSSRDTCTPYRNGSKYCEGRTRPSSCTENCPGCSALTFREEQCAAYNHT	650			
RC TISSUE-Brain;	RA Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S., Nagase T., Ohara O., Koga H., Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries.,		Qy	595 DLFKSFQGPMDMVTPRTGVAQPDQCLKTQARALGTYVLEPRVDTGPCSPDSSVVCQ	654			
RA	RA Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H., Nagase T., Ohara O., Koga H., Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries.,		Db	651 DLFKSFQGPMDMVTPRTGVAQPDQCLKTQARALGTYVLEPRVDTGPCSPDSSVVCQ	710			
RA	RA EMBL; AK173001; BAD32279.1; GO; GO:0004222; F:metalloendopeptidase activity; IEA. GO; GO:000508; P:proteolysis and peptidolysis; IEA.		Qy	655 GRCIHAQCDRTIGSKKRFKFDKCMVCGDGSCKQSFSRKFRYQYNNVVTIPAGATHILY	714			
RA	RA InterPro; IPR005586; ADAM_cysteine. InterPro; IPR010294; ADAM_spacer1. InterPro; IPR001590; Pept_M12B. InterPro; IPR000825; Pept_M_Zn_BS. InterPro; IPR000808; TSP1. InterPro; IPR000805; TSP1. InterPro; IPR01421; Reprolysin; 1. InterPro; IPR01705; TSPREPEAT.		Db	711 GRCIHAQCDRTIGSKKRFKFDKCMVCGDGSCKQSFSRKFRYQYSDVVTIPAGATHILY	770			
RA	RA SMART; SM00608; ACR; 1. SMART; SM00209; TSP1. PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.		Qy	775 GPLAQPLTQLVAGNFDQDTLRYSSFPVPRPTSPSTPRPTQDWLHQAILRLRREWVA	834			
RA	RA PROSITE; PS50092; TSP1. PROSITE; PS50215; ADAM_MEPRO; 1. PROSITE; PS50092; TSP1. PROSITE; PS50209; TSP1. PROSITE; PS50090; TSP1. PROSITE; PS50091; TSP1. PROSITE; PS50092; TSP1. PROSITE; PS50093; TSP1. PROSITE; PS50094; TSP1. PROSITE; PS50095; TSP1. PROSITE; PS50096; ADAM_spacer1; 1. PROSITE; PS50097; TSP1. PROSITE; PS50098; TSP1. PROSITE; PS50099; TSP1. PROSITE; PS50100; TSP1. PROSITE; PS50101; TSP1. PROSITE; PS50102; TSP1. PROSITE; PS50103; TSP1. PROSITE; PS50104; TSP1. PROSITE; PS50105; TSP1. PROSITE; PS50106; TSP1. PROSITE; PS50107; TSP1. PROSITE; PS50108; TSP1. PROSITE; PS50109; TSP1. PROSITE; PS50110; TSP1. PROSITE; PS50111; TSP1. PROSITE; PS50112; TSP1. PROSITE; PS50113; TSP1. PROSITE; PS50114; TSP1. PROSITE; PS50115; TSP1. PROSITE; PS50116; TSP1. PROSITE; PS50117; TSP1. PROSITE; PS50118; TSP1. PROSITE; PS50119; TSP1. PROSITE; PS50120; TSP1. PROSITE; PS50121; TSP1. PROSITE; PS50122; TSP1. PROSITE; PS50123; TSP1. PROSITE; PS50124; TSP1. PROSITE; PS50125; TSP1. 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DE	with thrombospondin motifs 4 (ADAM-TS 4) (ADAM-TS4) (Aggrecanase 1)	FT	DOMAIN	479	630	Spacer.
DE	(Fragment).	FT	DOMAIN	40	45	Poly-Ala.
GN	Name=Adamts4.	FT	METAL	154	154	Zinc (catalytic) (By similarity).
OS	Rattus norvegicus (Rat).	FT	ACT SITE	155	155	Zinc (catalytic) (By similarity).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT	METAL	158	158	Zinc (catalytic) (By similarity).
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	FT	METAL	164	164	Zinc (catalytic) (By similarity).
ON	"ADAMTS 4" (a disintegrin and metalloproteinase with thrombospondin motifs) is transintegrin and metalloproteinase with thrombospondin domains cleaved in beta-amylid treated rat astrocytes.",	FT	CARBOHYD	96	96	N-linked (GlcNAc. . .) (Potential).
[1]	SEQUENCE FROM N.A.	FT	CARBOHYD	474	474	N-linked (GlcNAc. . .) (Potential).
RP	STRAIN=Wildstar; TISSUE=Brain;	FT	SEQUENCE	630	630	MW, 63A428753167C7EF CRC54;
RC	Medline ID:20415831; PubMed=10961658; DOI=10.1016/S0304-3940(00)01285-4;	Query	Match	70.4 %	Score 3218;	DB 1; Length 630;
RX	Setoh K., Suzuki N., Yokota H.	Best Local Similarity	92.2 %	;	Pred. No. 4, e-199;	
RA	"ADAMTS 4" (a disintegrin and metalloproteinase with thrombospondin motifs) is transintegrin and metalloproteinase with thrombospondin domains cleaved in beta-amylid treated rat astrocytes.",	Matches	20;	Mismatches 29;	Indels 0;	Gaps 0;
RT	Neurosci. Lett. 289:177-180 (2000).	Qy	208 RRAKFKASLRSRVEVTLVVAADDKMKMAFGAGLKEYRLTMMAAAAKAKAFKHSIRAPVSVLVT	267		
RL	-I- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. May play an important role in the destruction of aggrecan in arthritic diseases. Cleaves aggrecan at the 392-Glu-Ala-393 site.	Db	1 RRTKFKASLRFVETLVAADDKMKMAFGAGLKEYRLTMMAAAAKAKAFKHSIRAPVSVLVT	60		
CC	-I- CATALYTIC ACTIVITY: Glutamyl endopeptidase, bonds cleaved include 392-Thr-Glu-Gly-Glu-Ala-Gly-Gly-Ser-377 in the interglobular domain of mammalian aggrecan.	Qy	268 RLVILGSGERGPQVCPGSAQTLSFCAWORGATNPEDSDPDHFDTAIFTTRODUGVSTC	327		
CC	-I- COFACTOR: Binds 1 zinc ion per subunit (By similarity).	Db	61 RLVILGSGQYVQPGVCPGSAQTLSFCPTWGLNPNDSDDHFDTAIFTTRODUGVSTC	120		
CC	-I- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).	Qy	328 DTLGMDADVGTVCDPARSCAVALVEDDGLQSAFTAAHELGHVNMLHDNSKPCISUNGPLSTS	387		
CC	-I- TISSUE SPECIFICITY: Brain specific.	Db	121 DALGNGAVGTVCDPARSCAVALVEDDGLQSAFTAAHELGHVNMLHDNSKPCANLINGQGSSS	180		
CC	-I- DOMAIN: The spacer domain and the TSP type-1 domain are important for a tight interaction with the extracellular matrix.	Qy	388 RHMVAPMAYHDPPEFWSPCSARFTDLDNGYGHQLLDKPEAHLPLPTPGKDYDADR	447		
CC	-I- DOMAIN: The spacer domain and the TSP type-1 domain are important for a tight interaction with the extracellular matrix.	Db	328 DTLGMDADVGTVCDPARSCAVALVEDDGLQSAFTAAHELGHVNMLHDNSKPCISUNGPLSTS	387		
CC	-I- SIMILARITY: Belongs to the peptidase M12B family.	Qy	448 QCOLTGFDPDSRSHCPCOLPPCPALWCGSHLNGHAMCCTKHSIWADETPCPGDAQACMGRCL	507		
CC	-I- SIMILARITY: Contains 1 disintegrin-like domain.	Db	241 QCOLTGFDPSSHCPCQDPPCPALWCGSHLNGHAMCCTKHSIWADETPCPGDAQACMGRCL	300		
CC	-I- SIMILARITY: Contains 1 TSP type-1 domain.	Qy	508 HMDQLQDFNPIOAGGGWPWGPGDCSRTCCGGVQFESSRDRDCTRTPVPGNGKCYCEGRTRFR	567		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	Db	301 HYDQLQDFNPIOAGGGWPWGPGDCSRTCCGGVQFESSRDRDCTRTPVPGNGKCYCEGRTRFR	360		
CC	EMBL: AB042272; BAB16474.1; EMBL: AB042271; BAB16473.1; DR	Qy	568 SCNTEDOPTGSAITPPEQCAAYNHDTDLFKSFPGPMDWVRYTGAPODQCKLTQARA	627		
CC	DR: AB042273; BAB16475.1; DR: AB042274; BAB16476.1; DR: HSSP; P07936; IISL.	Db	361 SCNTKNCPHGSALTFREREQCAAYNHDTDLFKSFPGPMDWVRYTGAPODQCKLTQARA	420		
CC	MEROPS: M12.221; DR: 621242; Adamts4.	Qy	628 LGYYYVLEPRAVVDGTPCSPDSSVCTQGRCHDRIIGSKKKFCKMVGDDGSGCSK	687		
CC	InterPro: IPR010294; ADAM_spacer1.	Db	421 LGYYYVLEPRAVADGTPCSPDSSVCTQGRCHDRIIGSKKKFCKMVGDDGSGCSK	480		
CC	InterPro: IPR0001762; Disintegrin.	Qy	688 QSGSFKEFRYGNVNTVTPAGATHYLVROQGNPQHHSIVYLALKLPDSYALNGEYLTIMP	747		
CC	InterPro: IPR0006025; Pept_M_Zn_BS.	Db	481 QSGSFKEFRYGSIVDVTTPAGRTHYLVROQGSGLIVYLALKLQDSYALNGEYLTIMP	540		
CC	InterPro: IPR0001590; PeptTidase_M12B.	Qy	748 PTDVYLPGAVSRYGDATASETLSGHGPLAQPLTQVLPAGNPNQTVRLRYSFFVPPRTP	807		
CC	InterPro: IPR000884; TSP1.	Db	541 STDVLPGAVSRYGDATASETLSGHGPLAQPLTQVLPAGNPNQTVRLRYSFFVPPRTP	600		
CC	InterPro: IPR000885; TSP 1.	Qy	808 STPRPTPQDWLHRRAQILEILRRPWAQRK	837		
CC	PFam: PF05986; ADAM_spacer1; 1.	Db	601 STPRPPQNWLRQRAEILEILRRPWAQRK	630		
CC	PFam: PF00441; Reprolysin; 1.	DR	with thrombospondin motifs 1 (ADAM-TS 1) (ADAM-TS 1) (ADAM-TS 1).			
CC	PRINTS: PRO1705; TEPREPEAT.	DR	DB with thrombospondin motifs 1 (ADAM-TS 1) (ADAM-TS 1) (ADAM-TS 1).			
CC	SNART; SM00209; TSP1; 1.	DR	DB with thrombospondin motifs 1 (ADAM-TS 1) (ADAM-TS 1) (ADAM-TS 1).			
CC	PROSITE: PS00215; ADAM_MPRO; 1.	DR	DB with thrombospondin motifs 1 (ADAM-TS 1) (ADAM-TS 1) (ADAM-TS 1).			
CC	PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.	DR	DB with thrombospondin motifs 1 (ADAM-TS 1) (ADAM-TS 1) (ADAM-TS 1).			
CC	PROSITE: PS50214; DISINTEGRIN_2; FALSE_NEG.	DR	DB with thrombospondin motifs 1 (ADAM-TS 1) (ADAM-TS 1) (ADAM-TS 1).			
CC	PROSITE: PS50092; TSP1; 1.	DR	DB with thrombospondin motifs 1 (ADAM-TS 1) (ADAM-TS 1) (ADAM-TS 1).			
CC	PROSITE: PS00142; ZINC PROTEASE_1.	DR	DB with thrombospondin motifs 1 (ADAM-TS 1) (ADAM-TS 1) (ADAM-TS 1).			
CC	Extracellular matrix; Glycoprotein; Hydrolase; Metalloprotease; Zinc;	DR	DB with thrombospondin motifs 1 (ADAM-TS 1) (ADAM-TS 1) (ADAM-TS 1).			
KW	Zymogen.	FT	PROTEIN_TER	1	1	Name=Adamts1;
FT	PRINTS: PRO1705; TEPREPEAT.	FT	CHAIN	<1	5	Rattus norvegicus (Rat).
FT	DR: SNART; SM00209; TSP1; 1.	FT	CHAIN	6	630	OS
FT	PROSITE: PS00215; ADAM_MPRO; 1.	FT	DOMAIN	6	232	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
FT	PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.	FT	DOMAIN	233	303	Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.
FT	PROSITE: PS50214; DISINTEGRIN_2; FALSE_NEG.	FT	DOMAIN	313	368	OC
FT	PROSITE: PS50092; TSP1; 1.	FT	DOMAIN	368	478	NCBI_TaxID=10116;

[1]	RN	SEQUENCE FROM N.A.Wiley; TISSUE=Brain;	253	967	ADAMTS-1.
	RP	STRAIN=Sprague-Dawley; TISSUE=Liver;	253	475	Metalloprotease.
	RC	MSDBLINE=20304099; Published=10847486;	476	558	Disintegrin-like.
	RA	Diamonds I.; Luebhi M.; Reichen J.;	559	614	TSP type 1_1.
	RA	"Induction of a disintegrin and metalloprotease with the thrombospondin type I motif (ADAMTS)"; Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.	616	724	Cy-rich.
[2]	RT	"Cloning of the rat ADAMTS-1 gene and its down regulation in endothelial cells in cirrhotic rats.,"	725	857	Spacer.
	RT	Liver 20:165-172(2000).	854	910	TSP type-1_2.
	RL	-1- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. Has angiogenic inhibitor activity (By similarity). Active metalloprotease, which may be associated with various inflammatory processes as well as development of cancer cachexia. May play a critical role in follicular rupture (By similarity).	911	967	TSP type-1_3.
	RN	SEQUENCE OF 18-967, FROM N.A.Wiley; TISSUE=Liver; MSDBLINE=20304099; Published=10847486;	914	198	Poly-Arg.
	RC	Diamonds I.; Luebhi M.; Reichen J.;	194	198	Cysteine switch (Potential).
	RX	"Cloning of the rat ADAMTS-1 gene and its down regulation in endothelial cells in cirrhotic rats.,"	205	205	Zinc (catalytic) (By similarity).
	RA	Liver 20:165-172(2000).	401	401	Zinc (catalytic) (By similarity).
	RT	-1- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. Has angiogenic inhibitor activity (By similarity). Active metalloprotease, which may be associated with various inflammatory processes as well as development of cancer cachexia. May play a critical role in follicular rupture (By similarity).	402	402	By similarity.
	CC	CCATYLIC ACTIVITY: Cleaves aggrecan at the 1683-Glu- -Leu-1684 site, within the chondroitin sulfate attachment domain.	405	405	Zinc (catalytic) (By similarity).
	CC	CCOPACTOR: Binds 1 zinc ion per subunit (By similarity).	411	411	Zinc (catalytic) (By similarity).
	CC	-1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).	547	547	N-linked (GlcNAc. . .) (Potential).
	CC	-1- INDUCTION: Down-regulated in endothelial cells derived from cirrhotic liver.	720	720	N-linked (GlcNAc. . .) (Potential).
	CC	-1- DOMAIN: The spacer domain and the TSP type-1 domains are important for a tight interaction with the extracellular matrix.	764	764	N-linked (GlcNAc. . .) (Potential).
	CC	-1- PTM: The precursor is cleaved by furin endopeptidase (By similarity).	782	782	N-linked (GlcNAc. . .) (Potential).
	CC	-1- SIMILARITY: Belongs to the peptidase M12B family.	945	945	N-linked (GlcNAc. . .) (Potential).
	CC	-1- SIMILARITY: Contains 1 disintegrin-like domain.	21	21	I->V (in Ref. 2).
	CC	-1- SIMILARITY: Contains 3 TSP type-1 domains.	26	31	KPSSQ -> RSRSQ (in Ref. 2).
	CC	CC- SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	49	49	Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;	72	72	V -> A (in Ref. 2).
	CC	CC- Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;	79	79	R -> P (in Ref. 2).
	CC	CC- 37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92	249	249	L -> TR (in Ref. 2).
	CC	CC- 35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89	262	265	R -> G (in Ref. 2).
	CC	CC- Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;	607	607	TMLV (in Ref. 2).
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	936	936	S -> F (in Ref. 2).
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	962	962	L -> V (in Ref. 2).
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	962	962	I -> T (in Ref. 2).
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Best Local Similarity 49.5%; Pred. No. 9.8e-131; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Matches 415; Conservative 137; Mismatches 217; Indels 69; Gaps 16;
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	37 LLLLAS-LLPSARLA-SPDREELVPEPKLGSVLPAGLICRQAGETL 92
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	35 MLLILLASITMLLCVGRGHRGPRTEEDELVLP---SLERARCHDSTTLLRDAFGQQL 89
	CC	CC- DB 967 AA: F93C864F6DCDB4CP CRCS64;	967	967	Query Match 47.3%; Score 2161.5; Pred. No. 9.8e-131; Length 967;
	CC				

Db	563	GPWGPGDCCSRTCGG3YQYTMRECDNEVPRNGCKYCEGRVYRSCNIECDPNDNGKTFP	622	DR	Pfam: PF00090; TSP 1; 3
Qy	584	EEQCAATNHRDLFKSPGPMDWPRYTGVAPODQCKLTCAORALGYYYLEPRYVDGTP	643	DR	PRINTS; PR01705; TSP1REPEAT.
Db	623	EEQCAARNEFSKASFGNEPTVEMTPKAGVSEPKDRCKLTCAAKGIGYFFVLPQKVVDGTP	682	DR	SMART; SM006108; TSP1; 1.
Qy	644	CSPDSSSVYCOGRCTHACCDRITGSKERKFDKCMVCGDGSGCSKOSFSFRKFRYGNVV	703	DR	PROSITE; PS50215; ADAM_MEPRO; 1.
Db	683	CSPDSSSVYCOGRCTHACCDRITGSKERKFDKCMVCGDGSGCSKOSFSFRKFRYGNVV	742	DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Qy	704	TIPAGATHLYRQOGNPHRS--IYLALKLPDSYALNGETMLMSPFTDVYLPGAVSLRY	761	KW	Integrin.
Db	743	TIPAGATNNEVKHNRPRSRNSFLAIRAADGTYINGNFTLSTLEQDLYTKGTV-LRY	801	SQ	SEQUENCE 967 AA; C6349B5D8CBFBA24 CRC64;
Qy	762	SGATAASETLSGCHGPLAQPLTQVLYVAGNPQDTRLRSFVPRPT-PSTPPTPTPQOWL	818	Query	Match 47.3%; Score 2160.5; DB 2; Length 967;
Qy	802	SGSSAALETRIRSRSPSLKEPLTQVLYMCHALRPKIKTYFMKCKTDENAIPTFSENV	859	DR	Best Local Similarity 49.5%; Pred. No. 1.1e-130; Indels 69; Gaps 16; Matches 415; Conservative 137; Nismatches 217;
Db	811	RESULT 10	913	Query	37 LILLIAS--LIPSBALIA--SPLPREEREVPEKLNGSYLPGSGAPARILCRLQAFGETL 92
Qy	968EJ2	Q6B8EJ2 PRELIMINARY; PRT; 967 AA.	914	DR	35 MLLLILASITMLLCYRGRPTDEELVLP---SLERARCHGTSLLRDAFGQOL 89
AC	Q6B8EJ2;	AC: 25-OCT-2004 (TREMBurrel. 28, Created)	915	Qy	93 LLLEBODSGVQVEGLTIVQVQGAPELGGAE-----PGTYLTGTINGDPEVASL 142
DT	Q6B8EJ2;	DT: 25-OCT-2004 (TREMBurrel. 28, Last annotation update)	916	DR	90 HKLQDSDGTLAPGTLQYGRSP---GSEAOHLDPTSDLAHCYFSGTIVNGDPSAAAL 145
DT	Q6B8EJ2;	DT: 25-OCT-2004 (TREMBurrel. 28, Last annotation update)	917	Qy	143 HWDGGALLGTVYQYGAELHQP-----LEGTP--NSAGGGPAHILRKSPASQGQP 192
DE	Q6B8EJ2;	DE: A disintegrin and metalloproteinase with thrombospondin motifs 1.	918	DR	146 SLCEG--VRGAFYLOQEEFFIQOPAPAVATERLYPAEPEEKSIAAPPFRHILRRRGSG-GA 203
GN	Q6B8EJ2;	GN: Rattus norvegicus (Rat).	919	Qy	193 MCNV-----KAPLGSPSP---RPR-----RAKRFAISLRFVETL 223
OS	Q6B8EJ2;	OS: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	920	DR	204 KCGVMDDEBTLPPTNSGRESQNTPDQWPLRNPPTPQAGAKPTGPGSTRKKFVSSPRYVETM 263
OC	Q6B8EJ2;	OC: Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	921	Qy	224 VVADDKMAAFAFGAGMCRYLITMMAAAKAKPHPSIRNPVSILVTRKLVFSSGEGPQVGP 283
OC	Q6B8EJ2;	OC: Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	922	DR	264 LYADQSNADFHGSGLKHYLTLFSVARYFPHPSINSISLVVVKLIVYEEQKGPETVS 323
OX	Q6B8EJ2;	OX: NCBI TaxID:10116;	923	DR	284 SAAQTLSRSPCAWQRGHTNPEDSDPDEFTDAILFTRDLCGTVCDTGLMADVGTVCDPAR 343
RN	Q6B8EJ2;	RN: SEQUENCE FROM N.A.	924	DR	324 NAALTLNFNCWSQKQONSPSDRDPVYTDTAIIFTRDLCGSHTCDDLGMDVGTVCDPSR 383
RP	Q6B8EJ2;	RP: TISSUE=Lung;	925	Qy	344 SCRIVEDGLQQAFTAHELGHVNMHNDSKPC1SINGPLSTSRSVHMAPYHDPPEP 403
RX	Q6B8EJ2;	RX: DOI=10.1073/pnas.242603899; PubMed:12477932; Last sequence update)	926	DR	384 SCSVIEDGLQQAFTAHELGHVNMHNDSKPC1SINGPLSTSRSVHMAPYHDPPEP 442
RA	Q6B8EJ2;	RA: Strausberg R.D., Fengold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klaunser R.D., Collins F.S., Wagner L., Sherman C.M., Schaefer C.M., Blatt N.K., Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.F., Jordan H., Moret B., Rubin G.M., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M.M., Soares M.B., Bonaldo M.W., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshikyu S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Millahy S.J., RA	927	Qy	404 WSPCSARFPTTDFDNGYGHCLLDKPEAHLHPVTFCKDYDADRCOLTFGPDSSRCPQL 463
RA	Q6B8EJ2;	RA: Rodriguez S., McEwan P.J., McKernan K.R., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villacon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton R., Kettman J., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Greenblatt J.W., Butterfield Y.S., RA	928	DR	443 WSPSSAINTSFLDNGHECLMDKQPQKPLPSDLPTLYDANRQOFTFGEBESTCPDA 502
RA	Q6B8EJ2;	RA: Rodriguez A.C., Grimwood J., Skalska U., Smailus D.E., Schein J.E., Jones S.J., Marra M.A.; Jones S.J. Marra M.A.; RTR: "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	929	Qy	524 GPNGPWNQCSRTGGVQFSSRPTVPRNGSKYCEGRTRRFRSNCNTEDCPTGSAALTFR 583
RA	Q6B8EJ2;	RA: Krzywinski M.I., Skalska U., Smailus D.E., Schein J.E., Schein J.E., RTR: "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	930	DR	563 GPNGPWNQCSRTGGVQFSSRPTVPRNGSKYCEGRTRRFRSNCNTEDCPTGSAALTFR 622
RN	Q6B8EJ2;	RN: SEQUENCE FROM N.A.	931	Qy	584 EBQZAYNHTDLEFSFPPGMDWPRYTGVAPODQKLTCAORALGTYVBLPRVYDCTP 643
RC	Q6B8EJ2;	RC: TISSUE=lung;	932	DR	623 EBQZAYNHTDLEFSFPPGMDWPRYTGVAPODQKLTCAORALGTYVBLPRVYDCTP 682
RA	Q6B8EJ2;	RA: Director MGC Project; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.	933	Qy	644 CSPDSSVYQGRCTHAGDRIGSKKEDKCMVCGGDSGCKSKSGFRKPYGYNNVV 703
RU	Q6B8EJ2;	RU: Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.	934	DR	683 CSPDSTSVCQGQCVTKAGCDRILDSKKEDKCGVCGNNSTRCKISGTVTSTRGHDIV 742
EMBL	Q6B8EJ2;	EMBL: BC080237; ARH80237.1; Pinterein-mediated signaling pathway; IBA.	935	Qy	704 TIPAGATHILVROQGNGPHRS--IYLALKLPDSYALNGETLIMPSPDVTVLPGAVSRLY 761
DR	Q6B8EJ2;	DR: GO: GO:0007229; Pinterein-mediated signaling pathway; IBA.	936	DR	743 TIPAGATNIEVKHRNPGRSGNRNSFLATRAADGTYILNENFTLSTLEQDLYTGTV-TRY 801
InterPro	Q6B8EJ2;	InterPro: IPR010229; ADAM_cysteine.	937	Qy	762 SGATASSETLSGHHGPIAQLPTLQVLYAGNFQDTLRLYSFFVPRPT-PSTPRTPTQDWL 818
InterPro	Q6B8EJ2;	InterPro: IPR001520; Peptidase_M12B.	938	DR	802 SGSSAALERIRSPSLKEPLTQVLYMGEHLRPKIYTFMKCKTTEPENAIPTFSEWW 859
InterPro	Q6B8EJ2;	InterPro: IPR006035; Pept_M_Zn_BS.	939	DR	RESULT 11
InterPro	Q6B8EJ2;	InterPro: IPR008084; TSP1.	940	DR	AT51_MOUSE
PFam	Q6B8EJ2;	PFam: PF05986; ADAM_spacer_1.	941	DR	
PFam	Q6B8EJ2;	PFam: PF01562; PEP_M12B_Propep_1.	942	DR	
PFam	Q6B8EJ2;	PFam: PF01421; Reprolysin_1.	943	DR	

ID	ATSL_MOUSE; STANDARD;	PRT;	968 AA.
AC	P97857; 054768;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	ADAMTS-1 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS 1) (ADAM-TS1).		
DB	Name="Adams1";		
GN	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=129/SvJv;		
RX	MEDLINE=98110583; PubMed=9951751; DOI=10.1006/geno.1997.5064;		
RA	Kuno K., Lizasa H., Ohno S., Matsushima K.;		
RT	"The exon/intron organization and chromosomal mapping of the mouse ADAMTS-11 gene encoding an ADAM family protein with TSP motifs.";		
RL	Genomics 46:466-471(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97150761; PubMed=995297; DOI=10.1074/jbc.272.1.556;		
RA	RAKADA N., Nakashima B., Fujiki F., Ichimura F.;		
RA	Matsushima K.;		
RT	"Molecular cloning of a gene encoding a new type of metalloproteinase-disintegrin family protein with thrombospondin motifs as an inflammation associated gene.";		
RT	RT		
RL	J. Biol. Chem. 272:556-562(1997).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Limb, and Mammary Gland;		
RX	MEDLINE=223188257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins P.S., Wagner L., Shemesh C.M., Schuler G.D.,		
RA	Klauschl S.P., Zeerberg B.H., Buetow K.H., Schaeffer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,		
RA	Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaido M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters K.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalona D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Pahey J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakley R.W., Touchman J.W., Green P.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,		
RA	Schneicher A., Schein J.B., Jones S.J.M., Marra M.A.,		
RA	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";		
RT	RT		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903 (2002).		
RN	[4]		
RP	CHARACTERIZATION, AND MUTAGENESIS OF GLU-403.		
RX	MEDLINE=99306557; PubMed=10373500; DOI=10.1074/jbc.274.26.18821;		
RA	Kuno K., Terashima Y., Matsushima K.;		
RT	"ADAMTS-1 is an active metalloproteinase associated with the extracellular matrix.";		
RT	J. Biol. Chem. 274:18821-18826 (1999).		
RN	[5]		
RP	FUNCTION, AND INDUCTION.		
RX	MEDLINE=20389568; PubMed=10930576; DOI=10.1016/S0014-5793(00)01854-8;		
RA	Kuno K., Okada Y., Kawashima H., Nakamura H., Miyasaka M., Ohno H.,		
RA	Matsushima K.;		
RT	"ADAMTS-1 cleaves a cartilage proteoglycan, aggrecan.";		
RL	FEBS Lett. 478:241-245 (2000).		
RN	[6]		
RP	FUNCTION, AND INDUCTION.		
RX	MEDLINE=20243757; PubMed=10781075; DOI=10.1073/pnas.080073497;		
RA	Robker R.L., Russell D.L., Espy L.L., Lydon J.P., O'Malley B.W.,		
RA	Richards J.S.;		
RT	"Progesterone-regulated genes in the ovulation process: ADAMTS-1 and		

ACT SITE	403	403	Zinc (catalytic) (By similarity).
METAL	406	406	Zinc (catalytic) (By similarity).
METAL	412	412	(Potential).
CARBONYD	548	548	N-linked (Gln/Asn. . .) (Potential).
CARBONYD	721	721	N-linked (Gln/Asn. . .) (Potential).
CARBONYD	765	765	N-linked (Gln/Asn. . .) (Potential).
CARBONYD	783	783	N-linked (Gln/Asn. . .) (Potential).
CARBONYD	946	946	N-linked (Gln/Asn. . .) (Potential).
MUTAGEN	403	403	E->Q: Loss of activity.
CONFLICT	335	335	N -> S (in Ref. 2).
CONFLICT	425	425	T -> S (in Ref. 2).
SEQUENCE	968	AA:	105841 MW: 428BD5499.B6C1 CRC64;
Query	Match	47.2%	Score 2158; DB 1; Length 968;
Best Local Similarity	49.4%	Pred. No. 1.7e-130;	
Matches	414;	Mismatches 221; Indels 68; Gaps 16;	
Qy	37	LILLILAS-L-LUPSLARIA--SPLPRBEEIVYYPEKINGSVLPGSGAPARLLCRLQAFGETL	92
Qy	35	MULLILASITMLCARGAHGRTEEDELVPLSLERA--PGHDSTTTL-RLDAFGQQL	90
Qy	93	LLEELBODSGVQVEGLTVQYLGQAEPELIGGAE-----GSEAQHLDPTGDLAHCYTSGTGNDGQSAAL	142
Qy	143	HWDGALLGIVLQYRGAELHQLPLEG-----GTP--NSAGGPGGAHLRKRSKPSAGQGP	192
Qy	147	SLC6G-VRGAFYLIQGEBEFFIQAPGVATERLAPAVPEEESSARPQPHILRRRGSG-GA	204
Qy	193	MCNV-----KAPLGSSPPPR-----RAKRPAISLSRFEVETL	223
Db	205	KCGIMDDETLPTSDISRPESQNTRNQWPYRDPFPQDAGKPSGPGSTRKKRKTVSSPPRYVETM	264
Qy	224	VVADDKMAAFHGAQLKRYLTITMAAAKAKHPSIRNPVSLIVVTRVILSGSGEPPQVGP	283
Db	325	NAALTLRNFCNWOQHNSPSDRPEHYDTAILTRQDLCGSHTCDTLGMDVGTCDPSR	384
Qy	385	SAATLRLSFCAWQAGLNTPDSOPDHDTAILTRQDLCGYSTCDTLMGMDVGTCDPAR	343
Qy	386	EDDGLQAAFTTAHELGHYTFNMHDNSRCPISNGPLSTSRYMAPUMAHYDPEEP	403
Db	404	WSPCISAREFTDFLDNGYGHCLDKEPEAHLPLPVTFGKDYDADRCQLTGFBDPSRHCPQL	463
Qy	444	WSPCISAXMVTFLDNGHGECLMDPQNPYKPLPSDLPGLTYLDANRQCFTEGEESEKHCPDA	503
Qy	464	PPPCACALWCSGHINGHAMCOTKHSKSPWADGTPCGBAQACNGRCRCLHMQLQDFNIPQGGW	523
Db	504	ASTCTTLCWTCGTCGGLVTCOTKHPFWADETSQCGKCNKTDMKHPATPYHGSW	563
Qy	524	GPWGPNGDCSPTCQSGYQFSSRDTCPVRNGGKTYCEGSRTRFRSCNTEDCPCTGSAUTER	583
Db	564	GPWGPNGDCSRTCGGGVQYTMRECDNPVKPGKGYCEGRVTRSCNTEDCPNNGTFR	623
Qy	584	EEQCAAYNHRDTFLKSFPGPMWDWRYTYGAPOQCKLTQARALGTYYVLEPRPVUDGTP	643
Db	624	EEQCEAHNEFSKASFGNEPTEWTPYAGYSPKURCKLTCEAKIGYFFVLPQKVYDGT	683
Qy	704	TPAGATHILYRQGNGHRS - IYIALKLKDGDSYALNGEYTIMSPDTPDVLPAVSLRY	761
Db	744	TIFAGATIIEVKHNRORGSRNGNFTLAFRAHDGTYTILNGNFTLSEQLQTYKCTV-IRY	802
Qy	762	SGATAASSTLSSHPGLAQLTQVAGNPDTRIYSFVPRPTPS-TPRPTQDWL	818
Db	803	SGGAALEIRISPSPLKEPLTQVLMGHALRKTFYTMKCKTESFNAIPTSEWV	860

RESULT 12	ATSI_HUMAN	STANDARD	PRT;	967 AA.
	ID ATSLI_HUMAN			
	AC Q9UH8; Q9UH8; Q9UH83; Q9UP80;			
	DT 30-JUN-2000 (Rel. 39, Created)			
	DT 16-OCT-2001 (Rel. 40, Last sequence update)			
	DT 25-OCT-2004 (Rel. 45, Last annotation update)			
	DB ADAMTS-1 precursor (BC 3.4 24.-) (A disintegrin and metalloprotease with thrombospondin motifs 1) (ADAM-TS 1) (ADAM-TS 1) (METH-1).			
	DE Name=ADAMTS1; Synonyms=KIAA1346, METH1;			
	GN OS Homo sapiens (Human).			
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
	OC NCBI_TAXID=9606;			
	OX			
	RN [1]	SEQUENCE FROM N.A.		
	RP			
	RA Casares C., Pritchard M.A., Retivill X., Arbones M.L.;			
	RA "Cloning, characterization and mapping on human chromosome 21 of the			
	RT orthologue of murine Adams-1."			
	RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
	RN [2]	SEQUENCE FROM N.A., AND FUNCTION.		
	RP			
	RC TISSUE=Heart;			
	RX MEDLINE=993167466; PubMed=10418512; DOI=10.1074/jbc.274.33.23349;			
	RA Vazquez F., Hastings G., Ortega M.-A., Lane T.F., Oktemur S.,			
	RA Lombardo M., Iruela-Arispe M.L.;			
	RA Rosenthal A., Thierauch K.H.;			
	RT "METH-1, a human ortholog of ADAMTS-1, and METH-2 are members of a new			
	RT family of proteins with angio-inhibitory activity.";			
	RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
	RL J. Biol. Chem. 274:23349-23357(1999).			
	RN [3]	SEQUENCE FROM N.A.		
	RP			
	RC TISSUE=Endothelial cells;			
	RX MEDLINE=2047184; PubMed=10785405;			
	RA Glensie J.J., Schmitt A.O., Pilarsky C., Hinzmman B., Weiss B.,			
	RA Rosenthal A., Thierauch K.H.;			
	RT "Differential gene expression by endothelial cells in distinct			
	RT antigenic states";			
	RT Bur. J. Biochem. 267:2820-2830(2000).			
	RL DNA Res. 7:65-73(2000).			
	RN [4]	SEQUENCE FROM N.A.		
	RP			
	RC TISSUE=Brain;			
	RX MEDLINE=20181126; PubMed=10718198;			
	RA Nagase T., Kikuno R., Ishikawa K.-I., Hirotsawa M., Ohara O.;			
	RA "Prediction of the coding sequences of unidentified human genes. XVI. The complete sequences of 150 new cDNA clones from brain which code for large proteins in vitro."			
	RT DNA Res. 7:65-73(2000).			
	RL [5]	SEQUENCE FROM N.A.		
	RP			
	RC TISSUE=Brain;			
	RX MEDLINE=20288799; PubMed=10830953;			
	RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,			
	RA Park H.-S., Toyota A., Ishii K., Totski Y., Choi D.-K., Soeda E.,			
	RA Ohki M., Takagi T., Sakai Y., Taudien S., Bleichschmidt K., Polley A.,			
	RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,			
	RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,			
	RA Rosenthal A., Kudoh J., Shibuya K., Kawasawa K., Asakawa S.,			
	RA Shintani A., Sasaki T., Nagamine K., Mitsuhashi S., Antonarakis S.E.,			
	RA Minoshima S., Shimizu N., Nordseik G., Hornischer K., Brandt P.,			
	RA Schaefer M., Schoen O., Desario A., Reichard J., Kauer G., Bloecker H.,			
	RA Rausser J., Beck A., Klaiges S., Hennig S., Rieselmann L., Dagand E.,			
	RA Weinmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,			
	RA Lehrach H., Reinhard R., Yaso M.-L.,			
	RT "The DNA sequence of human chromosome 21."			
	RL Nature 405:311-319(2000).			
	RN [6]	SEQUENCE OF 418-967 FROM N.A.		
	RP			
	RC TISSUE=Melanoma;			
	RA Blum H., Bauersachs S., Newes H.-W., Weil B., Wiemann S.;			
	RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases			
	CC -1- FUNCTION: Cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover (By similarity). Has angiogenic inhibitor activity. Active metalloprotease, which may be associated with			
	CC			

various inflammatory processes as well as development of cancer

CC - cachexia. May play a critical role in cancer

CC - site, within the chondroitin sulfate attachment domain.

CC - COFACTOR: Binds 1 zinc ion per subunit (By similarity).

CC - SUBCELLULAR LOCATION: Secreted. Associated with the extracellular matrix (By similarity).

CC - DOMAIN: The spacer domain and the TSP type-1 domains are important for a tight interaction with the extracellular matrix.

CC - PTM: The precursor is cleaved by a furin endopeptidase (By similarity).

CC - SIMILARITY: Belongs to the peptidase M12B family.

CC - SIMILARITY: Contains 1 disintegrin-like domain.

CC - SIMILARITY: Contains 3 TSP type-1 domains.

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CC EMBL: AP170084; AP15317.1; -

CC EMBL: AP060152; ADP48080.1; ALT_INIT.

CC EMBL: AP07664; AP03772.1; -

CC EMBL: AE037767; BRA92584.1; ALT_INIT.

CC EMBL: AE001697; BRA955502.1; -

CC EMBL: AL162080; CRBB82413.1; -

CC PIR: TA7158; T47158.

CC HSSP: P07996; 11SLH.

CC MEROPS: M12.222; -

CC GeneW: HGNC:217; -

CC ADAMTS1.

CC DR InInvDB: HIX0016042; -

CC DR MIM: 605174; -

CC DR GO:0008237; F: metallopeptidase activity; TAS.

CC DR GO:0007229; P: integrin-mediated signaling pathway; TAS.

CC DR GO:0008285; P: regulation of cell proliferation; TAS.

CC DR InterPro: IPR006546; ADAM cysteine.

CC DR InterPro: IPR010254; ADAM_spacer1.

CC DR InterPro: IPR001502; Disintegrin.

CC DR InterPro: IPR002870; Peptidase_M12B_N.

CC DR InterPro: IPR006025; Pept_M_Zn_BS.

CC DR InterPro: IPR000834; TSP1.

CC DR InterPro: IPR000805; TSP_1.

CC DR PFM: PF05986; ADAM_spacer1; 1.

CC DR PFM: PF01562; Pept_M12B_propep; 1.

CC DR PFM: PF01421; Reprolysin; 1.

CC DR PRINTS: PR01705; TSP1REPEAT.

CC SMART: SM00209; TSP1; 3.

CC PROSITE: PS50215; ADAM_MEPRO; 1.

CC PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.

CC PROSITE: PS00142; ZINC_PROTEASE; 1.

CC EXTRACELLULAR_MATRIX; Glycoprotein; Heparin-binding; Hydrolase;

CC Metalloprotease; Repeat; Signal; Zinc_Zymogen.

CC SIGNAL_1

CC PROPEP_50

CC CHAIN_253

CC FT DOMAIN_253

CC FT DOMAIN_476

CC FT DOMAIN_559

CC FT DOMAIN_614

CC FT DOMAIN_617

CC FT DOMAIN_724

CC FT DOMAIN_725

CC FT DOMAIN_849

CC FT DOMAIN_854

CC FT DOMAIN_905

CC FT DOMAIN_908

CC FT SITE_198

CC FT METAL_401

CC FT ACT_SITE_402

CC FT METAL_405

CC FT METAL_411

CC FT CARBOHYD_547

CC FT CARBOHYD_720

CC FT CARBOHYD_764

CC FT CONFLICT_227

CC FT CONFLICT_468

CC FT CONFLICT_561

CC SQ SEQUENCE_967_AA: 105383 MW: C18389324741ED1 CRC64;

Query Match 46.7% Score 2135; DB 1; Length 967;

Best Local Similarity 49.5%; Pred. No. 5e-129; Mismatches 226; Indels 70; Gaps 18; Matches 415; Conservative 127; MisMatches 226;

QY 37 LLLILLASLPSLPSLARLAPSLPREEVIVPEKLGNSVLQSGAPARLICRQAFGETLIEL 96

Db 36 LLLIAAALLAIVASDLAGRSEEDDELVYVPELERA--PCHGT-TRL-RLHAFPQQLDIL 89

QY 97 BQDSGQVQEGLTVQYLGAPELLGA--PGT---YLTTGNGPESVASHWDGGA 148

Db 90 RPSSSEFLAPGFTLQNVRK---SGSPLPLPEPLDIAICFYSCTVNGDPESSAAALSICEG- 144

QY 149 LIGVLYQYRGAELHQLPSEGTPNSA-GSPGA-----HILRK 184

Db 145 VRGAFYLLGEAYFIPQLPAASEPLATAAPGKEPPAPLOPHLLRNRRQDVGGTCGVVDD 204

QY 185 -----SPASGQPMCMVYKAP---LGSPSPR-RAKRFAASLSRFVETLV 224

Db 205 PRPTGKAAETEDDEGTEGDEGQFQWSPDPAQDQVQGPTGTGSIRKRFVSSRYVETML 264

QY 225 VADDKMAAFAHFGAQLKRLTLLVAAAKAFAKHSIRNPVSLVTRVILGSGBGPQVQGPS 284

Db 265 VADQSMAEFHGSLKHYLTLSVAARLYKHSIRNSVSLVYKILVHDEQKGPETVSN 324

QY 285 AAQTLRSCFAWGLNTPEDDHDFTAILFTTRODUGVSTCDTLMADGVTVCDPARS 344

Db 325 AAUTLRFNFCNWKQOHNPSPDRDAEHDTAILFTTQDQGSSQRTDTLMADGVTVCDPSSR 384

QY 345 CATVEDDGLQSATTAASLGHENMHLIDNSKPCISANGPLSTSRYHNAAPVMAHVDPEPW 404

Db 385 CSVIEDDGLQAAITTAASLGHENMHPDAKQASLNS-VNQDQSHMNRASMLSNLDSHSQSN 443

QY 405 SPCOSARPTIDPLDNGYGHCLDKPEAPLHLPYTPGKDYDAHQCLTGFPSRHCQPLP 464

Db 444 SPCASATMITSFLDNGHGECLMKPQNPFLQPLPQTSYDANRQCOFTGDESKHCPDA 503

QY 465 PPGAAALWGSGLHNGHACQTKHSIWPADGTPCPGAQACNGGRCLHMDOQDFNIPQAGEWG 524

Db 504 SPCSTLWCTGTSGGVLVCQTKHFWPAQDTSGCEGKWCINGKCYNKTDKHFDTPFHGSWG 563

QY 525 PNPQPGDCSRTCGGYFSSRDTCTPFRNGSKYCEGRTRPFSCTEDCPTGSAALTRE 584

Db 564 MNPQPGDCSRTCGVQYTMRECDNPYKNGKXGVRTRSCNLDCPDINGKTERB 623

QY 585 EQGAYNHTDL-FKSFFGPMDDWPRYTIGVAPDQCKLTQARALGTYVLLERVVDGTP 643

Db 624 EQEAEHNEFSKASFGSGFA-VEWIPKYGAVSPKDRKLICQAKGIGTFFVLPQKVVDGTP 682

QY 644 CSPDSSSSVCGQGRCIHAGCDRIGSKEKFDKCMVCGAGSGCSKQSGSFRKFRYGTNNVV 703

Db 683 CSPDSTSVCVQGQCVKZAGCDRIDISSLKFFDKGVCGGNGSTCKKISSGSSVTSAKPYHDII 742

QY 704 TIPAGATHILVRQGPNPGRHS--IYLAALKLPGDSYALNGEYLTMPSPDVVLFGAVSRY 761

Db 743 TIPPTGATMIEVORNRQRSRNRNSFLAIKAADTYIINGDYLSTLBDIMYXGVV-LRY 801

QY 762 SGATAASLTSGHGPQALQIPIQVIAAGNPQDTTRLYSPFVPRPTPS-TPRPTPQDWL 818

Db 802 SGSSAALERIRRSFSPLKEPLTIQVLTGNALRPKIVTYFVKKKEESNAIPTFSANV 859

Q8NE26	PRELIMINARY;	PRT;	967 AA.	
ID	Q8NE26;			
AC	Q8NE26;			
DT	01-OCT-2002 (TREMBrel. 22, Created)			
DT	01-OCT-2002 (TREMBrel. 22, Last sequence update)			
DT	01-MAR-2004 (TREMBrel. 26, Last annotation update)			
DE	A disintegrin and metalloprotease with thrombospondin motifs-1, proprotein.			
Name=ADMITS1;				
Homino	Batoids (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	Homino			
OX	TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RX	MEDLINE=22388357; Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaeffer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marsisina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Urdin T.B., Toshiyuki S., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullally S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heilcon E., Kettman M., Madden A., Rodriguez S., Sanchez A., Whiting M., Rubin A.C., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Stalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Matra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RA	Director MCG Project to the EMBL/GenBank/DBJ databases.			
DR	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC036515; AAH36515.1; -.			
DR	HSSP; P07936; 11SL.			
DR	GO; GO:0004222; F:metalloendopeptidase activity; IEA.			
DR	GO; GO:0006508; P:integrin-mediated signaling pathway; IEA.			
DR	InterPro; IPR000586; ADAM_cysteine.			
DR	InterPro; IPR010394; ADAM_spacer1.			
DR	InterPro; IPR001128; Cytochrome P450.			
DR	InterPro; IPR001590; Peptidase_M12B.			
DR	InterPro; IPR002670; Peptidase_M12B_N.			
DR	InterPro; IPR006025; Pept_M_Zn_BS.			
DR	InterPro; IPR000884; TSP1.			
DR	InterPro; IPR00885; TSP1.			
DR	Pfam; PF05986; ADAM_spacer1.			
DR	Pfam; PF01562; Pept_M12B_propep; 1.			
DR	Pfam; PF01421; Reptolysin; 1.			
DR	Pfam; PF00090; TSP1; 3.			
DR	PRINTS; PRO1705; TSP1REPEAT.			
DR	SMART; SM00608; ACR; 1.			
DR	PROSITE; PS50215; ADAM_MEPRO; 1.			
DR	PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.			
DR	PROSITE; PS50092; TSP1; 3.			
DR	PROSITE; PS01142; ZINC_PROPEPTIDE; UNKNOWN_1.			
KW	Integrin; Metalloprotease; Prostate.			
SEQUENCE	967 AA, 105387 MW,			
Query Match	46.5%	Score 227;	DB 2;	Length 967;
Best Local Similarity	49.4%	Pred. No. 1.e-12;		
Matches 414;	Conservative 127;	Mismatches 227;	Indels 70;	Gaps 18;
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Boerboom D., Russell D.J., Richards J.S., Sirois J.;			

Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP541975; AAN17331.1; -

DB 637 KKESENIA PTESEWV 651

Repeat; Signal; Zinc; zymogen. Potential.

FT SIGNAL 1 17 By similarity.

FT PROPEP 18 212 By similarity.

FT CHAIN 213 950 ADAMTS-15.

FT DOMAIN 213 427 Metalloprotease.

FT DOMAIN 428 515 Disintegrin-like.

FT DOMAIN 516 571 TSP type-1 1.

FT DOMAIN 572 700 Cys-rich.

FT DOMAIN 701 838 Spacer.

FT DOMAIN 839 895 TSP type-1 2.

FT DOMAIN 896 949 TSP type-1 3.

FT SITE 174 174 Cysteine switch (Potential).

FT METAL 361 361 Zinc (catalytic) (By similarity).

FT ACT SITE 362 362 Zinc (catalytic) (By similarity).

FT METAL 365 365 Zinc (catalytic) (By similarity).

FT METAL 371 371 Zinc (catalytic) (By similarity).

FT CARBOHYD 141 141 N-linked (GlcNAc . .) (Potential).

FT CARBOHYD 591 591 N-linked (GlcNAc . .) (Potential).

FT CARBOHYD 623 623 N-linked (GlcNAc . .) (Potential).

FT CARBOHYD 679 679 N-linked (GlcNAc . .) (Potential).

FT SEQUENCE 950 AA: 103286 MW: 5DFEBE18285CCC3B CRC64;

Query Match 41.9%; Score 1915; DB 1; Length 950;

Best Local Similarity 46.3%; Pred. No. 7.4e-115;

Matches 381; Conservative 123; Mismatches 267; Indels 52; Gaps 16;

Query 37 LLLLIASLPSARLAAASPAPREEEVPPERLNGSVL-----PGSAPARLICLQAF 88

Db 1 MLLGLGILTLAPAGRTAGGSEPEREVVVPRLDPPDINGRRYYWRGPEDSGDQGLIQLTAF 60

Query 89 GBTLLIELEODSGVQVEGLTVQYLGQAPE--LLGGAEP--GTYLTGTINGDPEVASLHWD 145

Db 61 QEDFTYHLTDDAQFLAPAPASTEHVLVPLGQLTGESSDILRCPFSGDYNMNEPDSFATSLC 120

Query 146 GGALLGVLYQYGAELHLOPLEGGCTPNSA--GGPAQHILRK---SPASQGEMCNV-- 196

Db 121 GG-LRGAFTYGRGAETVISPQPNASAPAAQRNSQAHLLQRRGYPGGPSDPTSRCYASG 179

Query 197 -----KAPLGSPPSPR--RAKRFASLSPRFVETLVADKMAAFHGAGLK 239

Db 180 WNPAILRLADPYKPRERAGFGESSRSRRSGRAKRFVSPYVETLVADSMVKEPHGADLB 239

Query 240 RYLLTWAIAAKAFRPSIRNPVSLVTVRLVLSGEGSPQVGBSAACTLRSFCAQRLG 299

Db 240 HYLLTLLATRRLYRHPSPILNPINVYKVLLLRDSDGKVTGNAALTIRNFCAWQKL 239

Db 300 NTPEDSPDHFDTAILTRDLCGVSTCDTGMDVGTCDPASCAVTEYDGLQSAFTA 359

Db 300 NKVSDKRPPEYNTDAILTRDLCGATTCDDGTLPSAFTT 359

Query 360 AHELGIVFNMLHDNSKPCISLNGPLSTSRYMAPYMAHNDPEEPWMSPCASRFITDFLNG 419

Db 360 AHELGIVFNMPHDNVKVEVFGKL-RANHAMSPTLIQIDRANPMSACGAAITDLSG 418

Query 420 YGHCLLDKPKEARPLHLPVTEPGKDYDADRCQCLTGFPSRHCQPLPPPCAAIWCSGHLNG 479

Db 419 HSDPCLLQPSKTPSLPDPGLASATYLSQOCLEAFGVSKEPEM-QYCTKLUWCTGAKGQ 477

Query 480 ANCQTKHSQSWADGTPCGDAQACMGGRGLMDQDENTPQAGGNGPWPQNGDCSRTCGG 539

Db 478 MYCQTRHPPWADGSTSCSGKLCLKGACYERHLNKHVD--GSWAKWDPGPSCSRTCGG 535

Query 540 VQFSSRDTCPYPRNGGKTCBGRTRPRSCNTEDCP-TGSALTFRREQCA--YNHRTD 595

Db 536 VQARRQCTNPFPAANGSKTCGYRKYRSCNLEPCFSSASGSFSREBQCEAFNGNNHSTN 595

Query 596 LFKSFPGPMDWPRYTGAPDQCKLTCQARALGYTLEPRVVDGTCPSPDSSSYCQG 655

Db 596 RLTL---AVAVWPKYSGSPRDKCLCRANGTGYFVTLAPKVVDGTLCSFDSTSVCQG 652

Query 656 RCIHAGCDRIIGSKKKFKFVKCMYCGDGGCGSKOSGSFRKFRGYNNVVTPAGATHILVR 715

Db 653 KC1KAGCDDNLGSKRFKRCGCGDNRSCCKVTKLFTKPMEGNYTFVAPGASSIDR 712